

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number 2015

TO: Ruixiang Li

Location: REM/4D75/4C70

Art Unit: 1646

Monday, August 08, 2005

Case Serial Number: 10/626126

From: Edward Hart

Location: Biotech-Chem Library

REM-1A55

Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Li,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart



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STIC-Biotech/ChemLib

168995

From:

Li, Ruixiang

Sent:

Friday, July 29, 2005 4:06 PM

To:

STIC-Biotech/ChemLib

Subject:

Sequence search of Application No.10/626,126

Please do a standard search on:

(i). SEQ ID NO: 9 against commercial amino acid databases.

(ii). SEQ ID NOS: 6 and 9 against commercial nucleic acid databases.

Thank you very much!

Ruixiang Li GAU 1646 REM 4D75 Mail Box 4C70 (571) 272-0875

STAFF USE ONLY

Searcher:
Searcher Phone: 2Date Searcher Picked up: Searcher Picked:
Date Completed:
Searcher Prep/Rev. Time:
Online Time:

Type of Search

S/L:____Oligomer:___ Encode/Transl:____

Structure#:_____ Text:___ Inventor:____ Litigation:___ Vendors and cost where applicable

STN:_______
DIALOG:_____
QUESTEL/ORBIT:____

QUESTEL/ORBIT:______LEXIS/NEXIS:______SEQUENCE SYSTEM______

WWW/Internet:____
Other(Specify):____

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Run

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                                                                                                                               August 5, 2005, 10:32:28 ; Search time 777 Seconds (without alignments) 9811.087 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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Copyright (c) 1993 - 2005
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Listing first 45 summaries
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H4 Subtype
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Sequence 11, Appli
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Sequence 26, Appl
Sequence 1, Appli
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FUDLication No. US20040248252A1

GENERAL INFORMATION;

APPLICANT: Lovenberg, Timothy

APPLICANT: Lovenberg, Timothy

TITLE OF INVENTION: DNAS Encoding Mammalian Histamine Receptor Of The H4 St

FILE REPRENCE: PRD-0032

CURRENT APPLICATION NUMBER: US/10/626,445

FRICR RAPLICATION NUMBER: 09/790,849

PRIOR APPLICATION NUMBER: 60/202

PRIOR PLING DATE: 2000-05-31

PRIOR FILING DATE: 2000-05-31

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PATENTIN VERSION 3.2

SEQ ID NO 6
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US-09-875-076-13

US-09-875-076-13

US-10-205-133-13

US-10-205-133-13

US-10-205-078-13

US-10-21-21-13

US-10-22-165-11

US-10-626-13-13

US-10-13-13-13

US-10-13-13-13

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Oy 1141 CCAGCACTTCACAGACCCAGTCAGTATCTTCTTGA 1176		; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype; FILE REFERENCE: PRO-0033; CURRENT APPLICATION NUMBER: US/10/626,126; CURRENT FILIGATION NUMBER: 2003-07-23; CURRENT FILIGATION DATE: 2003-07-23	; PRIOR APPLICATION NUMBER: 09/790,849 ; PRIOR APPLICATION NUMBER: 60/208,260 ; PRIOR PILING DATE: 2000-05-31	; NUMBER OF SEQ ID NOS: 2/ ; SOTWHARB: PatentIn version 3.2 ; SEQ ID NO 6 ; LENGTH: 1176	rtus	Query Match 100.0%; Score 1176; DB 21; Length 1176; Best Local Similarity 100.0%; Pred. No. 0; Matches 1176; Conservative 0; Mismatches 0; Indels 0; Gaps	1 ATGICGARGICTRACGGCACTGACGICTTGCCACTGCTCAAGTCCCCTTGGCATTT	61 TTAATGTCCCTGCTTGCTTTTGCTATAACGATAGGCAATGCTGTTGTGTCATTTTAGCCTTT	Oy 121 GTACAGAACCTTAGACATCGAAGTAATTATTTTTTTTTT	GACTICTICGIGGGGGTGTCATCTCCATICCTCTGACTGG 	Oy 241 AATTTTGGAAGTGGAATCTGCATGTTTTGGCTCATTACTGACTATCTTTTGTGCACAGCA 300 Db 241 AATTTTGGAAGTGGAATCTGCATGTTTTTGGCTCATTACTGACTATCTTTTGTGCACAGCA 300	QY 301 TCCGTCTACAGTATTGTCCTCATTAGCTACGATACCAGTCAGT	Oy 361 CGTTATAGAGCACACTGGCATCCTGAAAATTGTTGCTCAAATGGTGGTGGTTGG 420 161	OY 421 ATACTGGCTTTCTTGGTCAATGGCCCAATGATTCTGGCATTCTTGGAAGAACAGC 480	OY 481 ACCAACACAGAGAGTGCGAGCTTGGTTACTTGTTACTGGTACATCCTCGCCATTACA 540	Oy 541 GCATTCTTGGAATTCCTGCTCCTTGGTGGTCTATTTCAGTGTACAGATTTAC 600
61 TIBATGICCCTGCTTGCTTTTGCTATAACGATAGGCAATGCTGTGGTCATTTTAGCCTTT 120 	121 GTAGCAGAAACCTTAGACATCGAAGTAATTATTTTTTTTT	241 AATITIGGAAGIGGAATCIGCAIGITIGGCICATIACIGACIATCITIGIGCACAGCA 300 	301 TCCGTCTACAGTATTGTCCTCATTAGCTACGATACCAGTCAGT	361 CGTTATAGAGCACACACACTGGCATCCTGAAAATTGTTGCTCAAATGGGGGGTGTTTGG 420 	421 ATACTGGCTTTCTTGGTCAATGGCCCAATGATTCTGGCTTCGGATTCTTGGAAGAACAGC 480 	481 ACCAACACAGAGGAGTGCGAGCCTGGCTTTGTTACTGAGTGGTACATCCTCGCCATTACA 540 	541 GCATTCTTGGAATTCCTGCTCCCTGTCTCTGTGGTCTATTTCAGTGTACAGATTTAC 600	601 TGGAGCCTGTGGAAGCGTGGGAGTCTCAGTAGGTGCCCTAGCCACGCTGGATTCATCGCT 660	661 ACCTCTTCCAGGGGCACTGGACACTGCAGGCGTGGGTTGGCTTGTAGGACAAGTCTT 720 	CCTGGATTAAAGGAACCAGCCGCATCCCTTCATTCAGAAAGTCCACGAGGAAGAGCAGT	781 CTCCTGGTGTCCTTAAGGACTCACATGAGGGGGTACATCGCCTTCAAAGTGGGTTCC 840 	4. TTCTGCCGATCAGAAAGCCCAGTGCTTCACCAGAGAGCAGCACGTGGAGCTTCTCAGAGGGGGGGG	AGGAAGTAGCCAGGTGGCTAGCTGTCCTCAGAGTGCTTTTGCCATTTGCTGGCTCCG	TATTGCCTGTTCACATTGTTCTTTCAACTTATCGCAGAGGGGGGCCCCCAAATCGATT	TGGTACAGGCATTGCCTTTTTTTTTTTTTTTTTTTTTTT	CCTTTGTGCCACAGACGTTTCCAGAAGCTTTCTGGAAGATACTCTGTGTGACAAGCAA [

61 TTAATGTCCCTGCTTGCTTTTGCTATAACGATAGGCAATGCTGTGGTCATTTTAGCCTTT 120 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATTATTTTTTTT		TCCGTCTACAGTATTGTCCTCATTAGCTACGATACCAGTCAGT	CGTTATAGAGACACACTGGCATCCTGAAAATTGTTGCTCAAATGGTGGCTGTTTGG 	AFACTGGCTTTCTTGGAGGCCCAATGATTCTGGCTTCGGATTCTTGGAAGAGAGGG 48	481 ACCAACAGAGAGTGCGAGCTTGGTTTGTTACTGAGTGGTACATCCTCGCCATTACA 540	541 GCATTCTIGGAATTCCTGCTCCCTGTCTCCTTGGTGGTCTATTTCAGTGTACAGATTTAC 600 [601 TGGAGCCTGTGGAAGCGTGGGAGTCTCAGTAGGTGCCCTAGCCACGCTTGGATTCATCGCT 660 [661 ACCTCTTCCAGGGGCACTGGACACTCACGGAAACTGGGTTGGCTTGTAGGACAAGTCTT 720	721 CCTGGATTAAAGGAACCAGCCGCATCCCTTCATTCAGAAAGTCCACGAGGAAAGAGCGT 780	781 CTCCTGGTGTCCTTAAGGACTCACATGAGGGTAGTATCATCGCCTTCAAAGTGGGTTCC 840	841 TTCTGCCGATCAGAAGCCCAGTGCTTCACCAGAGAGAGCACGTGGAGCTTCTCAGAGGC 900	901 AGGAAGCTAGCCAGGTCGCTAGCTGTCCTCCAGTGCTTTTGCCATTTGCTGGGCTCCG 960	961 TAITGCCTGTTCACAATTGTTCTTCAACTTATCGCAGGGGGGGG	1021 TGGTACACCATAGCTTTTGGCTACAGTGGTTCAATTCACTTATTAATCCCTTTCTATAC 1080 1021 TGGTACAGCATAGCCTTTTGGCTACAGTGGTTCAATTCACTTATTAATCCCTTTCTATAC 1080	1081 CCTTTGTGCCACAGACGTTTCCAGAAGGCTTTCTGGAAGATACTCTGTGTGACAAAGCAA 1140	1141 CCAGCACCTTCACAGACCCAGTCATCTTGA 1176
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US-10-626-126-5

15 Sequence 5, Application US/10626126

15 Sequence 5, Application US/10626126

16 SEREAL INFORMATION:
17 GENERAL INFORMATION:
18 APPLICANT: Lovenberg, Timothy
18 APPLICANT: Lovenberg, Timothy
19 TILE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
17 TILE OF INVENTION: UNMBER: US/10/626,126
17 CURRENT FILING DATE: 2003-07-23
18 PRIOR PPLICATION NUMBER: 09/790,849
19 PRIOR PPLICATION NUMBER: 60/208,260
19 PRIOR PLING DATE: 2000-05-31
10 NUMBER OF SEQ ID NOS: 27
10 SOFTWARE: Patentin version 3.2
10 DATE: 2000-05-31
10 NUMBER OF SEQ ID NOS: 27
11 DATE: 2000-05-31
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                                                                         Sequence 5, Application US/10626445
Publication No. US20040248252A1
Publication No. US2004024825A1
| GENERAL INFORMATION:
| APPLICANT: Lovenberg, Timothy
| APPLICANT: Liu, Changlu
| TITLE OF INVENTION: DNAS Encoding Mammalian Histamine Receptor Of The H4 Subtype
| TITLE OF INVENTION: DNAS Encoding Mammalian Histamine Receptor Of The H4 Subtype
| TILLE OF TOWART OF 10 NOWBER: US/10/626,445
| CURRENT APPLICATION NUMBER: US/10/626,445
| CURRENT RILING DATE: 2001-02-22
| PRIOR PILING DATE: 2001-02-22
| PRIOR FILING DATE: 2001-05-31
| NUMBER OF SEQ ID NOS: 27
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Pred. No. 5e-295;
0; Mismatches 136; Indels
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Best Local Similarity 88.4%;
Matches 1040; Conservative
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1 ORGANISM: Mus musculus
US-10-626-445-5
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APPLICANT: LOVENDER, Timothy
APPLICANT: Lovenberg, Timothy
APPLICANT: Liu, Changlu
TITLE OF INVENTION: DNAE Encoding Mammalian Histamine Receptor Of The H4 Subtype
FILE REFERENCE: PRD-0034
CURRENT APPLICATION NUMBER: US/10/626,398
CURRENT FILING DATE: 2003-07-23
PRIOR APPLICATION NUMBER: 09/790,849
PRIOR FILING DATE: 2001-02-22
PRIOR PILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.2
SEQ ID NO 5
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Pred. No. 5e-295;
0; Mismatches 136;
US-10-626-398-5

Sequence 5, Application US/10626398

Publication No. US20050074841A1

GENERAL INFORMATION:

APPLICANT: Lovenberg, Timothy

APPLICANT: Liu, Changlu

TITLE OF INVENTION: DNAS Encoding M
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 88.4%;
Matches 1040; Conservative (
                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Mus musculus
US-10-626-398-5
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APPLICANT: Hedrick, Joseph A.
APPLICANT: Hedrick, Joseph A.
APPLICANT: Hedrick, Joseph A.
APPLICANT: Monse, Kelley L.
APPLICANT: Monse, Kelley L.
APPLICANT: Wind, Shelby P.
APPLICANT: Wind, Shelby P.
APPLICANT: Wind, Suke
TITLE OF INVENTION: Histermine receptor
FILE REFERENCE: CN01069
CURRENT APPLICATION NUMBER: US/09/812,216
CURRENT FILING DATE: 1999-10-07
PRIOR APPLICATION NUMBER: 09/414,010
PRIOR APPLICATION NUMBER: 09/414,010
PRIOR FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver: 2.1
SEQ ID NO.1
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) Patent No. US2002009B539A1
) GENERAL INFORMATION:
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Publication No. US20030017528A1
GENERAL INFORMATION:
APPLICANT: Chen, Kuoping
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
FILE REFERENCE: ARENO050
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CURRENT PILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US/09/875,076
CURRENT PILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-02-16
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-05-28
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FILING DATE: 1999-05-28
APPLICATION NUMBER: 60/137,131
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                                                                                                                                       APPLICANT: Fitzgerald, Laura
APPLICANT: Fitzgerald, Laura
APPLICANT: Fitzgerald, Laura
APPLICANT: Michalovich, David
APPLICANT: Ali, Yuan
TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
FILE REPRENCE: GP70655-221
CURRENT APPLICATION NUMBER: US/09/910,411
CURRENT FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/497,790
PRIOR APPLICATION NUMBER: 09/497,790
PRIOR PILING DATE: 2000-02-03
PRIOR PILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FRELSEQ for Windows Version 4.0
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ilarity 74.2%; Pred. No. 1.7e-202;
Conservative 0; Mismatches 295:
                                  Sequence 1, Application US/09910411
Patent No. US20020137054A1
GENERAL INFORMATION:
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ORGANISM: Homo sapien
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Matches 875; Conserv
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                                                                                                                                                                  655 GICTCTTCCAACATCTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT
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                                                                                                                                                                                                                                                                                                                                                          CCTTTGTGCCACAGACGTTTCCAGAAGGCTTTCTGGAAGATACTCTGTGTGACAAAGCAA
                                                                 661 ACCTCTTCCAGGGCACTGGACACTCACGCAGAACTGGGTTGGCTTGTAGGACAAGTCTT
                                                                                                                                                                                                                           CCTGGATTAAAGGAACCAGCCGCATCCCTTCATTCAGAAAGTCCACGAGGAAAGAGCAGT
                  TGGAGCCTGTGGAAGCGTGGGAGTCTCAGTAGGTGCCCTAGCCACGCTGGATTCATCGCT
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PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/141,448

PRIOR FILING DATE: 1999-06-29

PRIOR FILING DATE: 1999-06-29

PRIOR FILING DATE: 1999-09-29

PRIOR FILING DATE: 1999-09-29

PRIOR FILING DATE: 1999-09-29

PRIOR PRILING DATE: 1999-09-29

PRIOR APPLICATION NUMBER: 60/156,555

PRIOR APPLICATION NUMBER: 60/156,634

PRIOR PILING DATE: 1999-09-29

PRIOR FILING DATE: 1999-10-01

PRIOR FILING DATE: 1999-10-01

PRIOR PRILING DATE: 1999-10-01

PRIOR PRILING DATE: 1999-10-01

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PRIOR PRINGRAME: PRINGR
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Best Local Similarity 74.2
Matches 875; Conservative
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ORGANISM: Homo sapiens
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; Publication No. US20020132755A1
; GENERAL INFORMATION:
; APPLICANT: PEizer, Inc.
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; FILE REFERENCE: PC10963A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.9%; Score 669; DB 10; 74.2%; Pred. No. 1.7e-202; ive 0; Mismatches 295;
                 PRIOR APPLICATION UNDBER: 60/123,948
PRIOR PILING DATE: 1999-03-12
PRIOR PILING DATE: 1999-03-12
PRIOR PILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR PILING DATE: 1999-03-12
PRIOR PILING DATE: 1999-06-28
PRIOR PILING DATE: 1999-05-28
PRIOR PILING DATE: 1999-05-29
PRIOR PILING DATE: 1999-05-29
PRIOR PILING DATE: 1999-05-29
PRIOR PILING DATE: 1999-05-29
PRIOR PILING DATE: 1999-06-29
PRIOR PILING DATE: 1999-06-29
PRIOR PILING DATE: 1999-06-29
PRIOR PILING DATE: 1999-00-29
PRIOR PILING DATE: 1999-10-01
DR FILING DATE: 1999-03-12

DR APPLICATION NUMBER: 60/123,948

DR PLING DATE: 1999-03-12

DR APPLICATION NUMBER: 60/123,949

DR FILING DATE: 1999-03-12

DR APPLICATION NUMBER: 60/123,949

DR PLING DATE: 1999-03-03

DR PLING DATE: 1999-03-12

DR APPLICATION NUMBER: 60/131,114

DR PLING DATE: 1999-05-28

DR APPLICATION NUMBER: 60/136,439

DR APPLICATION NUMBER: 60/136,439

DR APPLICATION NUMBER: 60/136,439

DR APPLICATION NUMBER: 60/136,567

DR APPLICATION NUMBER: 60/137,127

DR FILING DATE: 1999-05-28

DR APPLICATION NUMBER: 60/137,137

DR FILING DATE: 1999-05-28

DR APPLICATION NUMBER: 60/137,137

DR PLING DATE: 1999-05-28

DR APPLICATION NUMBER: 60/137,137

DR PLING DATE: 1999-05-28

DR APPLICATION NUMBER: 60/136,437

DR APPLICATION NUMBER: 60/136,437

DR APPLICATION NUMBER: 60/136,437

DR APPLICATION NUMBER: 60/156,555

DR APPLICATION NUMBER: 60/156,555

DR APPLICATION NUMBER: 60/156,555

DR APPLICATION NUMBER: 60/157,280

DR APPLICATION NUMBER: 60/157,281

DR APPLICATION NUMBER: 60/157,281
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Best Local Similarity 74.2
Matches 875; Conservative
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ORGANISM: Homo sapiens
US-09-876-252-13
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Sequence 26, Application US/10290078
Publication No. US20030124596A1
GENERAL INFORMATION:
APPLICANT: Carroll, Joseph A.
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
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TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 10630, 10630, 10630, 10630, 10630, 10630, 10630, 10630, 10630, 10630, 10630, 10630, 10630, 10630, 10630, 10630, 10630, 10630, 10630, 10630, 10630, 10630, 10630, 10630, 10630, 10630, 10630, 10630, 10630, 10630, 1
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                                                                                               AGGAAGCTAGCCAGGTCGCTAGCTGTCCTCTGAGTGCTTTTGCCATTTGCTGGGCTCCG 960
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  TTCTCCCAATCAGATTCTGTAGCTCTTCACCAAAGGGAACATGTTGAACTGCTTAGAGCC
                                                                                                                                   AGGAGATTAGCCAAGTCACTGGCCATTCTCTTAGGGGTTTTTGCTGTTTTGCTGGGGCTCCA
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Pred. No. 1.7e-202;
0; Mismatches 295;
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Best Local Similarity 74.2%;
Matches 875; Conservative (
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US-10-290-078-26
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ORGANISM: Homo Sapien
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NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    941 TICIGCCGAICAGAAAGCCCAGIGCTICACCAGAGAGAGCACGIGGAGCTICICAGAGGC 900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421 ATACTGGCTTTCTTGGTCAATGGCCCAATGATTCTGGCTTCGGATTCTTGGAAGAACAGC 480
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Pred. No. 1.7e-202;
0; Mismatches 295; Indels
CURRENT APPLICATION NUMBER: US/10/052,193
CURRENT FILING DATE: 2002-01-17
PRIOR APPLICATION NUMBER: 0101223.6
PRIOR FILING DATE: 2001-01-17
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 74.2%;
Matches 875; Conservative
                                                                                                                                                                                                                                     1 TYPE: DNA
7 ORGANISM: Homo sapiens
US-10-052-193-1
                                                                                                                                                                                                          LENGTH: 1173
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Best Local Similarity 74.2%; Pred. No. 1.7e-202;
Matches 875; Conservative 0; Mismatches 295;
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 60/109,213
PRIOR FILING DATE: 1998-11-20
PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-05-28
PRIOR PILING DATE: 1999-05-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATTGCCTGTTCACAATTGTTCTTTCAACTTATCGCAGAGGGGAGCGCCCCAAATCGATT 1020
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                                                                              TCTTATAGAACTCAACATACTGGGGTCTTGAAGATTGTTACTCTGATGGTGGTCGTTGG 420
                                                                                                                                                                    GCATTCTTGGAATTCCTGCTCCCTGTCTCTTGGTGGTCTATTTCAGTGTACAGATTTAC 600
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       TCTGTATATAACATTGTCCTCATCAGCTATGATCGATACCTGTCAGTCTCAAATGCTGTG 360
                                                                                                                                          421 ATACTGGCTTTCTTGGTCAATGCCCCAATGATTCTGGCTTCGGATTCTTGGAAGAACAGC 480
                                                                                                                                                                                                                                    481 ACCAACACAGAGGAGTGCGAGCCTGGCTTTGTTACTGAGTGGTACATCCTCGCCATTACA 540
                                                                                                                                                                                                                                                               --TGAAGGTAGTGAATGTGAACCTGGATTTTTTTCGGAATGGTACATCCTTGCCATCACA 534
                                                                                                                                                                                                                                                                                                                                                                                                                       TGGAGCCTGTGGAAGCGTGGGAGTCTCAGTAGGTGCCCTAGCCACGCTGGATTCATCGCT 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GECTCTTCCAACAACTGTGGACACTCATTCAGAGGTAGATCTTCAAGAGAGATCTCTT 714
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                                                    CGTTATAGAGCACACACACTGGCATCCTGAAAATTGTTGCTCAAATGGTGGCTGTTTGG
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APPLICANT: Chen, Ruoping T.
APPLICANT: Dang, Huong T.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
FILE REFERENCE: ARRN0050
CURRENT APPLICATION NUMBER: US/10/272,983
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: US/09/417,044
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; Publication No. US20030148450A1
; GENERAL INFORMATION:
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181 GACTICTITGIGGGGGGGTGATCCCTITGIACATCCCTCACACGCTGITCGAATGG 301 TCTGTATATAACATTGTCCTCATCAGCTATGATCGATACCTGTCAGTCTCAAATGCTGTG 241 GAFTTTGGAAAGGAAATCTGTGTATTTTGGCTCACTACTGACTATCTGTTATGTACAGGA 361 TCTTATAGAACTCAACATACTGGGGTCTTGAAGATTGTTACTCTGATGGTGGCCGTTTGG 421 GTGCTGGCCTTCTTAGTGAATGGCCAATGATTCTAGTTTCAGAGTCTTGGAAGGA------TGAAGGTAGTGAATGTGAACCTGGATTTTTTTTCGGAATGGTACATCCTTGCCATCACA TCTGCATCGACAGAAGTTCCTGCATCCTTTCATTCAGAGAGACAGAGAGAAAGAGTAGT CTCCTGGTGTCCTTAAGGACTCACATGAGCGGTAGTATCATCGCCTTCAAAGTGGGTTCC 241 AATTTTGGAAGTGGAATCTGCATGTTTTGGCTCATTACTGACTATCTTTTGTGCACAGCA 361 CGTTATAGAGCACACACTGGCATCCTGAAAATTGTTGCTCAAATGGTGGCTGTTTGG 481 ACCAACACAGAGGAGGGGAGCCTGGCTTTGTTACTGAGTGGTACATCCTCGCCATTACA 535 TCATTCTTGGAATTCGTGATCCCAGTCATCTTAGTCGCTTATTTCAACATGAATATTTAT TGGAGCCTGTGGAAGCGTGGGAGTCTCAGTAGGTGCCCTAGCCACGCTGGATTCATCGCT 661 ACCTCTTCCAGGGGCACTGGACACTCACGCAGAACTGGGTTGGCTTGTAGGACAAGTCTT 655 Greictrecaacarergigakaeterreargaggragaerarerreaaggarerer 721 CCTGGATTAAAGGAACCAGCCGCATCCCTTCATTCAGAAAGTCCACGAGGAAAGAGCAGT TTAATGTCCCTGCTTTGCTATAACGATAGGCAATGCTGTGGTCATTTTAGCCTTT 61 477 541 715 775 841 835 901 895 961 955 1081 121 601 781 301 요 g ઠે 셤 셤 셤 ò 合 ò g ℰ 셤 Š 요 ò 요 ò g ઠે 요 ò g à g ò 8 8 g ઠ 셤 ે ઠે ઠે à

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APPLICANT: Liaw, Chen W
TILE OF INVENTION: Human Orphan G Protein Coupled Receptors
FILE REFERENCE: ARENOGSO
CURRENT APPLICATION NUMBER: US/10/393,807
CURRENT FILING DATE: 1999-10-12
FRIOR PELING DATE: 1999-10-12
FRIOR APPLICATION NUMBER: 60/100,213
FRIOR APPLICATION NUMBER: 60/100,213
FRIOR APPLICATION NUMBER: 60/120,416
FRIOR APPLICATION NUMBER: 60/123,946
FRIOR APPLICATION NUMBER: 60/136,436
FRIOR APPLICATION NUMBER: 60/136,437
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FRIOR APPLICATION NUMBER: 60/136,436
FRIOR FILING DATE: 1999-05-28
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.larity 74.2%; Pred. No. 1.7e-202;
Conservative 0; Mismatches 295; Indels 9;
                                           1141 CCAGCACCTTC---ACAGACCCAGTCAGTATCTTCTTGA 1176
                                                                CCTCTACCATCACACACAGTCGGTCAGTATCTTCTTAA 1173
                                                                                                                                                                                  Sequence 13, Application US/10393807; Publication No. US20330175891A1
SENERAL INFORMATION:
APPLICANT: Chen, Ruoping
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1 atgtcggagtctaacggcac.........cccagtcagtatcttcttga 1176 Gapop 10.0 , Gapext 1.0 US-10-626-126-6 1176 IDENTITY NUC Perfect score: Scoring table: Sequence:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Add30257 Mouse GPC Aa16750 Human his Aad401124 Human GP Aa18303 Human GP Ab280663 Human GP Ab280663 Human his Ab78739 Nucleotid Aa170800 Human his Aca93262 Human cDN Adg98759 Human cDN Adg98759 Human cDN Adg86374 Human cnd Adj88375 Novel hum Adp20167 Human end Adj88375 Novel hum Adg20167 Human end Adj88375 Human end Adj88375 Novel hum Adg20167 Human GPR Aai70982 Rat hista Aai70981 Mouse his Description SUMMARIES AAD01124 AAF83203 AAH24007 ABZ80663 AAQ7078739 AAT70980 ACA93262 ADG98759 ADP20167 ADQ75073 AAI66009 ADO30257 AA167750 AAA46023 ADJ26922 ADG86374 AAI70982 AAI70981 ADJ88375 ABS57063 5 10 10 10 Length DB 1173 1173 1173 1173 1173 1173 1173 1173 1173 1173 11227 Query Match 958.4 958.4 670.6 669 Score Result

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## ALIGNMENTS

Histamine H4 receptor; rat; antiasthmatic; antiallergenic; antiinflammatory; cardiant; circulatory; antidiabetic; laxative; diagnosis; gene therapy; ss. BP Rat histamine H4 receptor cDNA. (ORTH ) ORTHO-MCNEIL PHARM INC AAI70982 standard; cDNA; 1176 22-FEB-2001; 2001WO-US005914. 31-MAY-2000; 2000US-0208260P (first entry) Lovenberg T, Liu C; WPI; 2002-114339/15. P-PSDB; AAM50566. WO200192485-A1. Rattus rattus 18-MAR-2002 06-DEC-2001 AAI 70982; RESULT 1 AAI 70982 

encoding New mammalian histamine H4 receptor proteins and polynucleotides the proteins, useful in gene therapy for treating diseases where beneficial to elevate mammalian histamine H4 receptor activity.

Claim 4; Fig 5C; 92pp; English.

The present sequence is that of a cDNA clone encoding a rat histamine receptor of the H4 subtype. The cDNA was isolated from a rat spleen cDNA library. It shows 72.5% homology to the human H4 receptor coding region. The invention provides mammalian (human, mouse, rat and guinea pig) histamine H4 receptor nucleic acid molecules (see AAT70980-83) and polypeptides (see AAM50564-67). The nucleic acids have been expressed in

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recombinant host cells that produce active recombinant protein. The pharmacology of known histamine ligands is demonstrated. Mammalian histamine H4 receptor may be used in gene therapy for the treatment of diseases where it is beneficial to elevate mammalian histamine H4 receptor activity. Recombinant protein is useful for identifying modulators of the mammalian histamine H4 receptor. Such modulators may be useful for dagnosing, treating or preventing asthma, allergy, inflammation, cardiovascular and cerebrovascular disorders, non-insulin dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of the neuroendocrine system, stress and spasticity
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P-PSDB; AAM50565.
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The invention relates to human and mouse G protein-coupled receptors
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modulators of the mammalian histamine H4 receptor. Such modulators may b useful for diagnosing, treating or preventing asthma, allergy, inflammation, cardiovascular and cerebrovascular disorders, non-insulin dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of the neuroendocrine system, stress and spasticity
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Pred. No. 2.9e-300;
0; Mismatches 136;
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Matches 1040; Conservative
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                                                                                                                                                                                   TACTGTCTGTTCACAATTGTCCTTTCAACTTACCCCAGAACGGAACGCCCCAAATCGGTG
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Vassilatis D,
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Madisen L, Mcilwain KL, Pavlova MN,
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C (GPCRs) and mucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and mucleic acids of the invention, methods of treating, preventing or dispensing diseases c associated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; a transgenic mouse comprising a GPCR transgene or in an endogenous GPCR gene; calls derived from the transgenic mouse comprising a GPCR transgene or in an endogenous GPCR gene; calls derived from the transgenic mie; kits comprising several mice, each of which has mutation in a different GPCR gene of the invention; and kits comprising a mutation in a different GPCR gene of the invention; and kits comprising a GPCR nucleic acid. The GPCR publication of a which has comprising a GPCR nucleic acid. The GPCR publication of a wide variety of diseases including neurological disorders of the invention of a disease, disease, including neurological disorders of the colon or intestine of diseases including neurological disorders of the colon or intestine of seases including neurological disorders for the colon or intestine of surfacement of adjacrates of the adrenal gland; disorders for the adrenal gland; disorders (e.g., angiana, cardara carhythimia or myocardial infarction); muscular disorders (e.g., angiana, cardara carhythimia or surfacinal pour or osteoporosis); muscular disorders (e.g., angiana, cardara carhythimia or arthritis, gout or osteoporosis); muscular disorders (e.g., angiana, cardara disorders of the kidney, liver, lung, breast, ovary, uterain dal disorders of the kidney, liver, lung, breast, ovary, uterain dal disorders of the kidney, liver, lung, breast, dorthis contests), and disorders of the kidney, liver, lung, breast, and disorders of the present sequence and for this part did on form part of the present sequence and for this predict of the prise of the present dispersion; those sequences of the vidney of proton or or obtained in electronic format directly from W
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541 GCATTCTTGGAATTCCTGCTCCTGTCTCCTTGGTGGTCTATTTCAGTGTACAGATTTAC
                        601 ATGCTCTTGGAATTCCTGCTTCCTGTCATCTCTGTGGCTTATTTCAATGTACAGATTTAC
                                                                                                          ACCTCTTCCAGGGCCACTGGACACTCACGCAGAACTGGGTTGGCTTGTAGGACAAGTCTT
                                                                                                                                                               CCTGGATTAAAGGAACCAGCCGCATCCCTTCATTCAGAAAGTCCACGAGGAAAGAGCAGT
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                           ACCAACACAGAGGAGTGCGAGCCTGGCTTTGTTACTGAGTGGTACATCCTCGCCATTACA
                                                                                                                                                                                                      TGGAGCCTGTGGAAGCGTGGGAGTCTCAGTAGGTGCCCTAGCCACGCTGGATTCATCGCT
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                                                                                                                                                                                                                                                                                                                                                The invention provides an isolated histamine receptor, H4, which binds receptor can be expressed by standard recombinant methodology. Cells receptor can be expressed by standard recombinant methodology. Cells expressing H4 receptor protein at a detectable level can suppress cyclic adenosine monophosphate (CAMP) formation when contacted with the H4 receptor agonist. The H4 receptor and antibodies are used for identifying H4 receptor modulators. Modulation of histamine H4 receptors is useful controlled autoimmuse pathologies such as multiple sclerosis, type I diabetes, rheumatoid arthritis, cognitive and memory defects. The H4 receptor protein and nucleic acids are useful targets to identify drugs that are effective in treating disorders associated with histamine-regulated processes. Identification and isolation of H4 receptor provides for development of screening of molecules that interact with H4 receptors. Centeit variants of H4 can be used to diagnose an H4 associated disease as described above. The H4 receptor polynucleotide is useful to treat or provine a disorder associated with the function of H4 in peripheral blood
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                                                                                                                                                                                                                      New histamine receptor, termed H4 useful for detecting H4 (ant)agonists for treating transplanted organ rejection, asthma, allergy, multiple sclerosis and rheumatoid arthritis.
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histamine H4 receptor protein
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                                                                                                              Pausch MH;
                                                                  (AMHP ) AMERICAN HOME PROD CORP.
                                                                                                                                                                                                                                                                                                             Claim 13; Fig 1; 66pp; English
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23-AUG-2000; 2000US-0227567P.
13-NOV-2000; 2000US-0247855P.
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Matches 876; Conservative
                                                                                                              Blatcher M,
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The present invention describes transmembrane receptors, preferably human g protein coupled receptors (GPCR), for which the endogenous ligand is unknown (orphan GPCR receptors). More specifically the present invention relates to non-endogenous, constitutively activated versions of a human GPCR. These non-endogenous human GPCRs can be useful for the direct identification of candidate compounds as receptors agonists, inverse agonists or partial agonists for use as pharmaceutical agents. AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in the exemplification of the present invention
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1020 TGGTACAGCATAGCCTTTTGGCTACAGTGGTTCAATTCACTTATTAATCCCTTTCTATAC 1080 960 CCATTGTGTCACAAGCGCTTTCAAAAGGCTTTCTTGAAAATATTTTTGTATAAAAAAGCAA 1134 840 900 540 534 9 9 720 780 834 894 954 240 300 360 360 420 420 480 476 594 654 714 774 300 --TGAAGGTAGTGAATGTGGATTTTTTCGGAATGGTACATCCTTGCCATCAC GCATTCTTGGAATTCCTGCTCCCTGTCTCCTTGGTGGTCTATTTCAGTGTACAGATTTAC AGGAAGCTAGCCAGGTCGCTAGCTGTCCTCCTGAGTGCTTTTGCCATTTGCTGGGCTCCG TATTGCCTGTTCACAATTGTTCTTTCAACTTATCGCAGAGGGGGGCGCCCCAAATCGATT TGGTATAGAATTGCATTTTGGCTTCAGTGGTTCCAATTCCTTTGTCAATCCTCTTTTGTAT TCTGCATCGACAGAAGTTCCTGCATCCTTCATTCAGAGAGACAGAGGAGAAAGATAGT crcargririccicaagaaccaagargaaragcaaracaarrgcrirccaaaargggrircc TTCTGCCGATCAGAAAGCCCAGTGCTTCACCAGAGAGAGCACGTGGAGCTTCTCAGAGGC AGGAGATTAGCCAAGTCACTGGCCATTCTCTTAGGGGTTTTTTGCTGTTTTGCTGGGCTCCA TATICICIGITICACAATIGICCTITICATITITATICCTCAGCAACAGGICCTAAATCAGIT CCTTTGTGCCACAGACGTTTCCAGAAGGCTTTCTGGAAGATACTCTGTGACAAAGCAA 241 GATTTTGGAAAGGAAATCTGTGTATTTTGGCTCACTACTGACTATCTGTTATGTACAGGA TCTGTATATAACATTGTCCTCATCAGCTATGATCGATACCTGTCAGTCTCAAATGCTGTG TCTTATAGAACTCAACATACTGGGGTCTTGAAGATTGTTACTCTGATGGTGGCCGTTTGG GIGCTGGCCTTCTTAGTGAATGGGCCAATGATTCTAGTTTCAGAGTCTTGGAAGGA----GTCTCTTCCAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT CTCCTGGTGTCCTTAAGGACTCACATGAGCGGTAGTATCATCGCCTTCAAAGTGGGTTCC GACTTCTTCGTGGGTGTCATCTCCATTCCTCTACATCCCTCACACGCTGTTTAACTGG GACTTCTTTGTGGGTGTGTGTTCTCCTTTGTACATCCCTCACACGCTGTTCGAATGG 241 AATTTTGGAAGTGGAATCTGCATGTTTTGGCTCATTACTGACTATCTTTTGTGCACAGCA CGTTATAGAGCACAGCACACTGGCATCCTGAAAATTGTTGCTCAAATGGTGGTGGTTTTGG ATACTGGCTTTCTTGGTCAATGGCCCCAATGATTCTGGCTTCGGATTCTTGGAAGAACAGC ACCAACACAGAGGAGTGCGAGCCTGGCTTTGTTACTGAGTGGTACATCCTCGCCATTACA TGGAGCCTGTGGAAGCGTGGGAGTCTCAGTAGGTGCCCTAGCCACGCTGGATTCATCGCT ACCICITCCAGGGCACTGGACACTCACGCAGAACTGGGTTGGCTTGTAGGACAAGTCTT CCTGGATTAAAGGAACCAGCCGCATCCCTTCATTCAGAAAGTCCACGAGGAAAGAGCAGT 1173 CCAGCACCTTC - - - ACAGACCCAGTCAGTATCTTCTAGA 181 301 361 421 421 481 541 535 595 199 655 715 775 841 835 901 895 196 1021 1015 1081 1075 1141 1135 301 361 477 601 721 781 g g 셤 g ò 요 ò 유 ઠે 요 ે 용 ઠે 셤 ે 유 셤 g ठे 용 ଚ 셤 ⋧ 셤 ð 요 ઠે 음 ð 8 à કે

AAD01124 ID AAD01124 standard; cDNA; 1173 | XX

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                                                         Length 1173;
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Pred. No. 3.8e-206;
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                    Seguence 1173 BP; 294 A; 245 C; 231 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human orphan G protein-coupled receptors and the encoding cDNAs for use in the identification of G protein-coupled receptor agonists.
                                                                                                                    screening;
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/product= "hRUP7"
/note= "Human orphan G protein-coupled receptor"
                                                                                                                Human, orphan G protein-coupled receptor; GPCR; hRUP7; drug
transmembrane receptor; signal cascade; ss.
                                                                         Human orphan G protein-coupled receptor hRUP7 cDNA
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diseases, allergy and respiratory disease, sensory organ disorders, sleep disorders and hair loss. The PFI-013 protein and mucleic acid are useful in the diagnosis and treatment of the above conditions and also for screening drug candidates for the treatment of diseases associated with signal transduction. The antibodies are also useful for enrichment of eosinophils from mammalian, especially human blood and for detecting the
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                                                                                                                                                                                                                                                                                                                                                                                         Length 1173;
                                                                                                                                           Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
                                                                                                                                                                                                             Indels
                                                                                                                                                                          56.9%; Score 669; DB 4; L
74.2%; Pred. No. 3.8e-206;
cive 0; Mismatches 295;
                                                                                                        protein in biological samples
                                                                                                                                                                                            llarity 74.2%;
Conservative
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es 875; Conserv
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 TATTCTCTGTTCACAATTGTCCTTTCATTTTATTCCTCAGCAACAGGTCCTAAATCAGTT 1014
                                                                                                                                                                                                                                                                                                                                                                                                                                       G-protein coupled receptor; GPCR; PFI-013; antiallergic; antiasthmatic; antiinflammatory; vasotropic; antidiabetic; anorectic; cytostatic; human; osteopathic; neuroprotective; nootropic; dermatological; gynecological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sexual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This cDNA of NCIMB 41073 encodes a human G-protein coupled receptor (GPCR)-like polypeptide, designated PFI-013. The PFI-013 protein can be expressed by standard recombinant methodology. Antibodies and modulators of PFI-013 are useful in the manufacture of a medicament for treating allergic disorder, including extrinsic asthma, immunological disorders, such as intrinsic asthma, vasculitic granulomatous disease, interstitial and other pulmonary disease, including chronic obstructive pulmonary bowel disease and neoplastic and myeloproliferative diseases. They are also useful for treating obseity, diabetes, metabolic, neurological diseases, psychotherapeutics, uncapental disease, reproduction and sexual medicine, inflammation, cancer, tissue repair, dermatology, photoageing, skin pigmentation, cancer, tissue repair, dermatology, photoageing, skin pigmentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New G-protein coupled receptor-like polypeptide, polynucleotide for screening drug candidates for treating diseases associated with signal transduction e.g. allergic, inflammatory, pulmonary, neoplastic diseases.
                                                                                                      CCTTTGTGCCACAGACGTTTCCAGAAGGCTTTCTGGAAGATACTCTGTGTGACAAAGCAA
                                                                   TOGTATAGAATTGCATTTTGGCTTCAGTGGTTCAATTCCTTTGTCAATCCTCTTTTGTAT
                                                                                                                                                                            1176
                                                                                                                                                                                                                                                                                                                                                                                                        Human GPCR-like polypeptide, PFI-013 encoding cDNA
                                                                                                                                                                          CCAGCACCTTC---ACAGACCCAGTCAGTATCTTGA
                                                                                                                                                                                                    CCTCTACCATCACACACAGTCGGTCAGTATCTTCTTAA
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                                                                                                                                                                                                                                                                                                 standard; cDNA; 1173
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20-APR-2000; 2000GB-00009973.
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(PFIZ ) PFIZER INC.
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                                                                                                       AXOR35; human; G protein-coupled receptor; 7TM receptor; histamine H3 receptor homologue; infection; viral; bacterial; fungal; protozoan; H1V-1; H1V-2; pain; cancer; diabetes; obseity; anorexia; bulimia; osteoporosis; asthma; allergy; urinary retention; acute heart failure; hypotension; bypertension; angina pectoris; myocardial infarction; stroke; ulcer; migraine; vomiting; psychotic disorder; neurological disorder; anxiety; schizophrenia; manic depression; bipolar disorder; depression; delizium; dementia; severe mental retardation; dyskinesia; Parkinson's disease; Huntington's disease; Gilles de la Tourette's syndrome; lymphocyte; macrophage; eosinophil; neutrophil; function modulation; autoimmune disorder; pulmonary disorder; gene therapy; vaccine; drug screening; signal transduction; transgenic animal; drug discovery;
AGGAGATTAGCCAAGTCACTGCCCATTCTCTTAGGGGTTTTTTGCTGTTTTGCTGGGCTCCA
                            TATTGCCTGTTCACAATTGTTCTTTCAACTTATCGCAGAGGGGGGCCCCCAAATCGATT
                                                        TATICTCTGTTCACAATIGTCCTTTCATTTATTCCTCAGCAACAGGTCCTAAATCAGTT
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                                                                                                                                                                                                           CCAGCACCTTC --- ACAGACCCAGTCAGTATCTTCTTGA 1176
                                                                                                                                                                                                                            /product= "Human AXOR35"
/note= "G protein-coupled receptor"
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                                                                                                                                                                                                                                                                                                                  AAH24007 standard; cDNA; 1173 BP.
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03-FEB-2000; 2000US-00497790.
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Michalovich D, Morrow DM,
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P-PSDB; AAB73622.
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The invention relates to the human G protein-coupled receptor XXXX

(AAB3621), to CDNA encoding AXXR35 (AAB34006), and to AXXR35 fragments
and variants Like all G protein-coupled receptors. AXXR35 has
and variants Like all G protein-coupled receptors such
transmembrane domains and is involved in signal transduction. AXXR35 has
created to the human histamine H3 receptor. The invention also relates to
as the human histamine H3 receptor. The invention also relates to
capression vectors and host cells comprising AXXR35 bnA, to recombinant
expression vectors and host cells comprising AXXR35 bnA, to recombinant
cxpression of AXXR35, and to an AXXR35-specific antibody. AXXR35 proteins
and nucleotides may be used to treat a wide variety of disorders
and nucleotides may be used to treat a wide variety of disorders
cc including bacterial, fungal, protezoal and viral infections, particularly
HIV-1 or HIV-2 infections; pain; cancers; benign prostatic hypertension;
curinary retention; acute heart failure; hypotension; hypertension; and particularly cellification and delirium, demental, and severe mental
curinary retention; and dyskinesion, delirium, demental, and severe mental
cc pertoris; myocardial inferction; stroke; ulcers; migralne; vomiting;
manic depression, depression, delirium, demental, and severe mental
cc retardation, and dyskinesias, such as Parkinson's disease, Huntington's
disease or dilles de la Toucette's syndrome. AXXR35 proteins and
nucleotides may be used in screening compounds for their ability to
modulate AXXR35 activity or expression. Such AXXR35 proteins, nucleotides are also
cucionately useful for treating asthma, and inhibiting or promoting the
function of lymphocytes, macrophages, cosinophils or neutrophils in
asthmatic lung. AXXR35 proteins, nucleotides and antibiodies are useful for disponsing or determining susceptibility of an inmanial conding gene. AXXR35 incleoting also medical med
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180
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                                      treating cancer, autoimmune, pulmonary, cardiovascular and neurological disorders and for identifying modulators useful for treating asthma.
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Pred. No. 3.8e-206;
0; Mismatches 295; Indels
                                                                                                                                              Claim 2; Page 49-50; 54pp; English.
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#ATTGCCTGTTCACAATTGTTCTTTCAACTTATCGCAGAGGGGAGCGCCCCAAATCGATT 1020
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                                                                        ATACTGGCTTTCTTGGTCAATGGCCCAATGATTCTGGCTTCGGATTCTTGGAAGAACAGC 480
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New nucleic acid encoding antigenic part of human histamine receptor. useful for preparing antibodies, e.g. for treating-histamine related

Example 1; Col 27-28; 19pp; English.

SP;

Umland

Morse KL,

Monsma FJ,

Laz TM,

Behan JX, Hedrick JA, (SCHE ) SCHERING CORP

Wang S;

WPI; 2002-442063/47 P-PSDB; AB098629

99US-00414010 99US-00414010.

07-OCT-1999; 07-OCT-1999;

US6204017-B1 20-MAR-2001

"Histamine receptor"

Location/Qualifiers

sapiens

Homo Key

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This sequence represents the open reading frame for a human histamine receptor (HR) designated SP9144. The sequence was isolated by searching databases with the sequence of known G-coupled protein receptor (GCPR). The gene is used for recombinant production of HR and for preparing antibodies (Ab). These Ab are used to purify HR by immunoaffinity chromatography, in immunoassay of histamine receptor, to identify cDNA clones that express the receptor, as antagonist to block binding of histamine (for treating any histamine-associated disorder) and to generate anti-idiotypic antibodies. Agonists and antagonists of the HR protein can be used in the treatment of e.g. inflammation, asthma, allergy, atopic dermatitis, strok, myocardial infarction, migraine, chronic obstructive pulmonary disease, rheumatoid arthritis, multiple sclerosis, inflammatory bowel disease and psoriasis
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Best Local Similarity 74.2%; Pred. No. 3.8e-206;
Matches 875; Conservative 0; Mismatches 295;
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anti-asthmatic; anti-allergic; dermatological; cerebroprotective; stroke, anti-migraine; cardiant; anti-rheumatic; anti-arthritic; antiporiatic; anti-arthritic; antiporiatic; muroprotective; inflammation; asthma; allergy; atopic dermatitis; myocardial infarction; migraine; chronic obstructive pulmonary disease; rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;

psoriasis, receptor.

human; histamine receptor; gene; ds; chromosome 18; anti-inflammatory;

Human histamine receptor coding sequence.

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hormone secretion; gene;
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               CGTTATAGAGCACACACACTGGCATCCTGAAAATTGTTGCTCAAATGGTGGCTGTTTGG
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The present sequence encodes a human histamine receptor. The polypeptide is useful for identifying an agonist or antagonist of a mammalian of statement erceptor. It is useful as an antigen to elicit the production of antibodies. The histamine receptor polypeptide and polymuclectide are useful in the treatment and management of diseases such as inflammation, asthma, allergy, atopic dermatitis, stroke, myocardial infection, migraine, chronic obstructive pulmonary disease (COPD), rheumatoon arthritis, multiple sclerosis, inflammatory bowel disease and psoriasis. They are also useful for modulating intracellular second messenger pathway activated through histamine receptors (cyclic-AMP, calcium, inositol phosphate and mitogen activated protein (MAP) kinase), changes in cellular growth rate, secretion of hormones, receptor-stimulated Ca2+
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Best Local Similarity 74.2%; Pred. No. 3.8e-206;
Matches 875; Conservative 0; Mismatches 295; Indels
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                                                                /*tag= a
/product= "histamine receptor"
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Location/Qualifiers
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HEDRICK J A.
LAZ T M.
MONSMA F J.
MORSE K L.
UMLAND S P.
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Histamine H4 receptor; human; antiasthmatic; antiallergenic; antiinflammatory; cardiant; circulatory; antidiabetic; laxative; diagnosis; gene therapy; ss.

(ORTH ) ORTHO-MCNEIL PHARM INC

WPI; 2002-114339/15. P-PSDB; AAM50564.

Lovenberg T,

22-FEB-2001; 2001WO-US005914. 31-MAY-2000; 2000US-0208260P

WO200192485-A1

06-DEC-2001

Homo sapiens

Human histamine H4 receptor cDNA

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TGGTACAGCATAGCCTTTTGGCTACAGTGGTTCAATTCACTTATTAATCCCTTTCTATAC 1080
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The present sequence is that of cDNA clone pH4R encoding a human histanine receptor of the H4 subtype. The cDNA was isolated from a bone marrow cDNA library. The invention provides mammalian (human, mouse, rat and guinea pig) histanine H4 receptor nucleic acid molecules (see AANT0980-81) and polypeptides (see AAM50564-67). The nucleic acids have been expressed in recombinant host cells that produce active recombinant protein. The pharmacology of known histanine ligands is demonstrated protein. The pharmacology of known histanine ligands is demonstrated treatment of diseases where it is beneficial to elevate mammalian histanine H4 receptor activity. Recombinant protein is useful for identifying modulators of the human histanine H4 receptor. Such modulators may be useful for disgnosing, treating or preventing asthma, allergy, inflammation, cardiovascular and cerebrovascular disorders, non-insulin dependent disbetes mellitus, hyperglycemia, constipation, cardiovascular and cerebrovascular disorders.
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the proteins, useful in gene therapy for treating diseases where it is
beneficial to elevate mammalian histamine H4 receptor activity.
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Pred. No. 3.8e-206;
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2001US-00875076

The invention relates to a human G protein-coupled receptor (GPCR)
appearing as ABU92259-ABU92277 (encoded by CDNAs ACA93256-ACA92247) named
hARE-3, hARE-4, hARE-5, hRUP3, hRUP6, hRUP7, hGPCR27, hARE-1, hARE
-2, hPPR1, hC2A, hCHN3, hCHN8, hCHN8, hCHN9, hCHN10 and hRUF4.
Also included are a plasmid comprising a vector and one of the CDNAs
bove and a host cell comprising the plasmid. The GPCRs are useful for
the direct identification of candidate compounds as inverse agonists,
agonists or partial agonists. In vitro and in vivo systems incorporating
CPCRs is useful for elucidating and understanding the roles these
receptors play in the human condition, both normal and diseased, as well
as understanding the role of constitutive activation as it applies to
understanding the signalling cascade. The CDNAs are useful for making a
probe for dot-blot analysis against tissue mRNA and/or RT-PCR
identification of the expression of the receptor in tissue samples. The
present sequence is a CDNA encoding a GPCR of the invention 120 180 120 9 9 Novel endogenous, orphan, human G protein-coupled receptors useful for identification of modulators of the receptor and as research tools for understanding the role of the receptor in human body. 61 TTAATGTCCCTGCTTGCTATAACGATAGGCAATGCTGTGGTCATTTAGCCTTT 61 TITATGTCCTTAGTAGCTTTTGCTATAATGCTAGGAAATGCTTTGGTCATTTTAGCTTTT 1 ATGTCGGAGTCTAACGGCACTGACGTCTTGCCACTGACTCCTCAAGTCCCCTTGGCATTT <u> Argecagaractrarecarterentina de la argenativa de la argenativa de la receptado de la compositiva della compositiva del</u> Gaps 6 56.9%; Score 669; DB 8; Length 1173; 74.2%; Pred. No. 3.8e-206; ative 0; Mismatches 295; Indels Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other; Claim 25; Page 22; 54pp; English. Best Local Similarity 74.2 Matches 875; Conservative М 121 요 셤 ò 8 ઠ

Human; 88; gene; orphan G protein-coupled receptor; GPCR; hARE-3; hARE-4; hARE-5; hRUP3; hRUP5; hRUP7; hGPCR27; hARE-1; hARE-2; hPPR1; hG2A; hCHN3; hCHN4; hCHN8; hCHN9; hCHN10; hRUP4; signalling cascade.

Human cDNA encoding GPCR hRUP7.

(first entry)

16-JUL-2003

BP.

ADG98759 standard; cDNA; 1173

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11-MAR-2004

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                                                                 GTCTTCCAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTTTT
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The present invention provides novel human G protein-coupled receptor (GPCR) proteins and their encoding nucleic acids. The invention is useful for making a probe for dot-blot analysis and for RT-PCR identification of the expression of the receptor in tissue samples. The invention is also useful for identifying candidate compounds as inverse agonists, agonists or partial agonists and as research tools in determining the location of the receptors within the body. The present sequence is human orphan G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New cDNA encoding a human G protein coupled receptor, useful for making probe for dot-blot analysis against tissue-mRNA, and/or for RT-PCR identification of the expression of the receptor in tissue samples.
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                                                                                        Human; G protein-coupled receptor; GPCR; research tool; gene;
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The invention relates to an isolated G-protein coupled receptor polypeptide, AXOR35, (and its homologues and variants) and its encoding polypuclectide (and its homologues, variants, complements and RNA equivalents). Also included are an anti-AXOR35 antibody, an AXOR35 expression vector, producing a recombinant host cell by introducing the vector into a cell such that the host cell by introducing the the host cell expressing AXOR35, identifying/screening for agonists or antagonists of AXOR35 and inhibiting or promoting the function of lymphocytes, macrophages, eosinophils, or neutrophils in diseased tissue, by administering to the patient AXOR35 and sonists or antagonists. The agonist or antagonist identified is useful for treating a disease such as asthma, or for inhibiting or promoting the function of lymphocytes,
                                                                                                                                                                                                                                                                                 macrophage; eosinophil; neutrophil; infection; transplant rejection; gastrointestinal disorder; gastric ulcer; inflammatory bowel disease; from a disease; irritable bowel syndrome; vomiting; inflammation; atopic dermatitis; allergy; autoimmune disorder; rheumatoid arthritis; psoriasis; urcological disease; urinary retention; cardiovascular disease; myocardial infarction; hypotension; hypertension; pulmonary disorder; renal ischaemia; arteriosclerosis; atherosclerosis; psychosis; neurological disorder; migraine; anorexia; anxiety; schizophrenia; dyskinesia; Parkinson's disease; cancer; obesity; stroke; septic shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated G-protein coupled receptor polypeptide, AXOR35, useful for treating infections, gastrointestinal disorders, autoimmune disorders, urological diseases, cardiovascular diseases and cancer.
                                                                                                                                                                                                                                                                       Human; ss; gene; G-protein coupled receptor; AXOR35; lymphocyte;
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D, Morrow DM, Zhu Y;
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macrophages, eosinophils, or neutrophils in diseased tissue such as an asthmatic lung. AXOR35 or polynucleotide is useful in disgnostic assays, for identifying compounds that are agonists or antagonists of AXOR35, as vaccines, or for treating infections (bacterial, fungal, protozoan or viral infections), transplant rejection, gastrointestinal disorders (such as gastric ulcer), inflammatory bowel diseases (such as croin's disease), irritable bowel syndome, vomiting, inflammation (such as atopic dermatitis), allergy, autoimmune disorders (such as rheumatoid arthritis, psoriasis), urological diseases (such as urinary retention), protoension, pulmonary diseases (such as schonic obstructive pulmonary disease), cough, renal diseases (such as charing obstructive pulmonary disease), cough, renal diseases (such as renal ischaemia), artherosclarosis, atherosclarosis, psychotic and neurological disorders (such as migralne, anorexia, anxiety, schizophrenia), dyskinesias (such as Parkinson's disease), cancer, obesity, stroke, septic shock, graft versus host disease and osteoporosis. The present sequence is the cDNA
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56.9%; Score 669; DB 10;
Best Local Similarity 74.2%; Pred. No. 3.8e-206;
Matches 875; Conservative 0; Mismatches 295;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	AF358860 Rattus no	AF358859 Mus muscu	AC118386 Rattus no	AX301763 Sequence	AF307973 Homo sapi	AR142850 Sequence	AR391860 Sequence	AX109119 Sequence	AX139113 Sequence	BD015847 Novel pol	AF325356 Homo sapi	AF329449 Homo sapi	AY008280 Homo sapi	AY136745 Homo sapi	AJ298292 Homo sapi	BD097512 Novel gua	AB044934 Homo sapi	AX376577 Sequence	AX301229 Sequence
	ID	AF358860	AF358859	AC118386	AX301763	AF307973	AR142850	AR391860	AX109119	AX139113	BD015847	AF325356	AF329449	AY008280	AY136745	HSA298292	BD097512	AB044934	AX376577	AX301229
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/product="histamine H4 receptor"
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TYTKDCBPGFVPTBWYILTTTMLLBTLLPYLSYAYFRVOIYWSLWFRAALSRFCESHAGF
STTSSSASGHLHRAQVACRTSNFGIKESSAASRHSSESPRKGSILVSLRTHMNSSITAF
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ERPKSVWYSIAFWLQWFNSFVNPFLYFLCHRRFQKAFWKILCVTKQPALSQNQSVSS"
                                                                                                                                                                                                                                                                                                                                                           AF358859 1538 bp mRNA linear ROD 02-SEP-2001
Mus musculus histamine H4 receptor mRNA, complete cds.
AF358859
                                                                                                                                                         Unpublished

(Dases 1 to 1538)

Liu,C., Wilson,S., Kuei,C. and Lovenberg,T.W.

Liuctanision

Direct Submission

Submitted (12-MAR-2001) Molecular Pharmacology, The R.W. Johnson

Pharmaceutical Research Institute, 3210 Merryfield Row, San Diego,
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Comparison of human, mouse, rat, and guinea pig histamine
receptor suggests substantial species variation
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                                                                                                                                                                                                       On Nov 15, 2002 this sequence version replaced gi:23812823. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 236694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 217900: contig of 217900 bp in length
901 218000: gap of unknown length
901 214816: contig of 16816 bp in length
817 234916: gap of unknown length
917 234694: contig of 1778 bp in length.
Location/Qualifiers
1 . 236694:
/organism="Rattus norregicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.4%; Score 815.8; DB 2; 99.8%; Pred. No. 4.5e-235;
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clone_end:Sp6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA'
/db_xref="taxon:10116"
/clone="CH230-397N16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     end_sequence:BZ179483"
210891 2141
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complement (209467. .21
/note="clone_boundary
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2310. .3895
/note="wgs_contig"
103725. .105993
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    COMMENT
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CTTCCTGGATTAAAGGAACCAGCCGCATCCCTTCATTCAGAAAGGTCCACGAGGAAAGAGC 183694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183813 GCTACCTCTTCCAGGGGCACTGGACACTCACGCAGAACTGGGTTGGCTTGTAGGACAAGT 183754
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183693 AGTCTCCTGGTGTCCTTAAGGACTCACATGAGCGGTAGTATCATCGCCTTCAAAGTGGGT
                                                                                                                      184113 GTGCGTTATAGAGCACAGCACACTGGCATCCTGAAAATTGTTGCTCAAATGGTGGCTGTT
                                                                                                                                                                                    418 TGGATACTGGCTTTCTTGGTCAATGGCCCAATGATTCTGGCTTCGGAATTCTTGGAAGAAC
                                                                                                                                                                                                                                                                                                                                                               183993 AGCACCAACACAGAGGAGTGCGAGCCTTGTTACTTACTGAGTGGTACATCCTCGCCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                          ACAGCATTCTTGGAATTCCTGCTCCTGTCTCCTTGGTGGTCTATTTCAGTGTACAGATT
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                                                           GTGCGTTATAGAGCACAGCACACTGGCATCCTGAAAATTGTTGCTCAAATGGTGGCTGTT
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Mismatches
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Sequence 1 from Patent WO0185786.
AX301763
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YNIVLISYDRYLSVSNAVSYRTQHTGVLKIVTLMVAVWVLAFLVNGPMILVSESWKDE
GSECEPGFESEWYILAITSFLEFVIPVILVAXFNMNIYWSLWKRDHLESRCOSHPGITA
KSSNICGHSFRGRLSSRTSLASTEVPASFHSERQRRKSSLMFSRTKMNSNTIASKM
GSFSQSDSVALHQREHVELLRARRLAKSLAILLGVPRVCMAPYSLETIVLSFYSSATG
PKSVWYRIAFWLQWFNSFVNPLLYPLCHKRPQKAFLKIFCIKKQPLPSQHSRSVSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MPDTNSTINLSLSTRVTLAFFMSLVAFAIMLGNALVILAFVVDK
NLRHRSSYFFLNLAISDFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASV
                                                                                                                                                                                   TGGTACAGCATAGCCTTTTGGCTACAGTGGTTCAATTCACTTATTAATCCCTTTCTATAC 1080
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Bukaryogie...

Bukaryogie...

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Jones, P.G., Wu,S. and Betty,M.

Cloning of a novel histamine receptor

Upublished

Closes 1 to 1173)

Jones, P.G., Wu,S. and Betty,M.

Submission

Submission

Submission

Submission

Submission

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Location/Qualifiers
                                      AGGAGATTAGCCAAGTCACTGGCCATTCTCTTAGGGGTTTTTGCTGTTTGCTGGGCTCCA
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Homo sapiens histamine H4 receptor mRNA, complete cds.
AF307973
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    1173
/note="G protein coupled receptor"

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74.3%; Pred. No. 3.1e-191;
ive 0; Mismatches 294;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="histamine H4 receptor"
/protein_id="AAG32052.1"
/db_xref="G1:11141733"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
    AGGAAGCTAGCCAGGTCGCTAGCTGTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="18"
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SOURCE
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ACCESSION
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                       (SD)
Patent: WO 0185786-A 1 15-NOV-2001,
American Home Products Corporation
Location/Qualifiers
1. 1173
                                                                                          /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Behan, J.X., Hedrick, J.A., Laz, T.M., Monsma, F. Umland, S.P. and Wang, S.
Polynucleotide encoding a histamine receptor Patent: US 6204017-A 1 20-MAR-2001;
Location/Qualifiers
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Best Local Similarity 74.2%; Pred. No. 9.4e-191;
Matches 875; Conservative 0; Mismarches not.
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Sequence 1 from patent US 6204017.
AR142850
                                                                                                                                                                                                                                                                                                                             /organism="unknown"
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- F-F S S S S R R R R R R R R R R R R R R R	GCAGT  GTAGT  GTAGT  GTAGT  GTAGT  GTAGC  GAGGC  GAGGC  CTCCA  CTCCA  CTCCA  TATAC  TATAC		and Wang, S.  6613533-A 1 02-SEP-2003;  6613533-A 1 02-SEP-2003;  6613533-A 1 02-SEP-2003;  7173  rganism="unknown"  21_type="genomic DNA"  74.2%;

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Catarrhini; Hominidae; Homo.
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G-protein coupled receptor-like polypeptide
Patent: EP 109609-A 102-MAY-2001;
Pfizer Limited (GB) ; PFIZER INC. (US)
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/mol_type="unassigned DNA"
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Sequence 1 from Patent EP1096009.
AX139113
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Mammalia, Butheria, Primates;
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Pred. No. 9.4e-191;
0; Mismatches 295; Indels
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 74.2%;
Matches 875; Conservative (
                 Homo sapiens (human)
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DE Homo sapiens (human)
PN JP 201211889-A/1
PN JP 201211889-A/1
PD 07-AUG-2001
PP 27-OCT-2000 JP 2000329359
PR 29-OCT-1999 GB 9925641:4,20-APR-2000 GB 0009973:9 PI
BEAT PETER, MARK ANTONY OLAYLEE
PC C12N15/09, A61K39/00,A61K39/395,A61K48/00,A61P1/04, PC A61P11/06, A61P29/00,A61P31/00, A61P37/02,A61P37/08, PC A61P11/06, A61P11/06
                 Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
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larity 74.2%; Pred. No. 9.4e-191;
Conservative 0; Mismatches 295;
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                                                                                                           07-AUG-2001;
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                 Chordata;
Primates;
           Eukaryota; Metazoa; Chordate
Mammalia; Eutheria; Primatee;
1 (bases 1 to 1173)
Peter, B. and Olaylee, M.A.
Novel polypeptide
Patent: JP 2001211889-A 1 07
PFIZER INC
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               CGTTATAGAGCACACCACACTGGCATCCTGAAAATTGTTGCTCAAATGGTGGCTGTTTGG
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BD015847 Novel polypeptide. BD015847 BD015847.1 GI:22556984 JP 2001211889-A/1. Homo sapiens (human)

BD015847 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE

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                                                                              sapiens"
                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="18"
/map="18q11.2"
1. .1173
/gene="AXOR35"
       Location/Qualifiers
                                                                           organism="Homo"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1173)
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Mol., Pharmacol. 59 (3), 434-441 (2001)
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Zhu,Y., Michalovich,D. and Fitzgerald,L.R.
Direct Submission
Direct (30-NOV-2000) GlaxoSmithKline, 709
1539, King of Prussia, PA 19406, USA
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0; Mismatches 295;
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Submitted (15-DEC-2000) Human Genomics Research, Schering-Plough
Research Institute, 2015 Galloping Hill Rd., Kenilworth, NJ 07033,
USA
GECTCTTCCAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT
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Monsma, F.J. Jr., Wang, S., Behan, J., Laz, T.M., Greene, J.
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    .1173
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/mol_type="mRNA"
    /db_xref="taxon:9606"

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                                                     TICICCCAAICAGAITCTGIAGCICTICACCAAAGGGAACAIGTIGAACTGCTIAGAGCC 894
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1173)
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Direct Submission
Submitted (26-SEP-2000) Pharmacology, University of Toronto,
Taddle Creek Rd., Rm. 4353, Toronto, Ont M5S 1A8, Canada
Location/Qualifiers
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Nguyen, T., George, S.R., Lee, D.K., Cheng, R., Lynch, K.R. and
O'bowd, B.P.
Discovery of H4, a Novel Histamine Receptor
Unpublished
3 (bases 1 to 1173)
Nguyen, T., George, S.R., Lee, D.K., Cheng, R., Lynch, K.R. and
O'Dowd, B.F.
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                                                                                                                                                                                                                                                                                                            CCAGCACCTTC---ACAGACCCAGTCAGTATCTTCTTGA 1176
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|protein_id="AAL09297.1"
|db_xref="G1:15822541"
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                                            Euteleostomi,
                                                                                                                                                                 Direct Submission
Submitted (11-JAN-2001) O'Reilly M.A., Discovery Biology, Pfizer
Ltd, Ramsgate Road, Sandwich, Kent, CT13 9NJ, UNITED KINGDOM
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGCCAGATACTAATAGCACAATCAATTTATCACTAAGCACTCGTGTTACTTTAGCATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACTICTITIQIGGGIGIGATCTCCATTCCTTTGTACATCCTCACACGCTGTTCGAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGTCGGAGTCTAACGGCACTGACGTCTTGCCACTGCTCAAGTCCCCTTGGCATTT
                                                                                                H4 receptor on human eosinophils
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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6
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Best Local Similarity 74.2%; Pred. No. 9.4e-191;
Matches 875; Conservative 0; Mismatches 295; Indels
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Identification of a histamine
Role in eosinophil chemotaxis
Unpublished
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                                                                                                                                                                                                                                                                                                                                                             codon_start=1
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histamine receptor H.
Homo sapiens (human)
Homo sapiens
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O'Reilly, M.A.
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421 GFGCTGGCCTTCTTAGTGAATGGGCCAATGATTCTAGTTTCAGAGTCTTGGAAGGA----
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                                                                                                                                                                                                        541 GCATTCTTGGAATTCCTGCTCCCTGTCTCCTTGGTGGTCTATTTCAGTGTACAGATTTAC
                                                                                                                                                                                                                                                                                                                               TGGAGCCTGTGGAAGCGTGGGAGTCTCAGTAGGTGCCCTAGCCACGCTGGATTCATCGCT
                                                                                                                                                                                                                                                                                                                                                                    661 ACCTCTTCCAGGGCACTGGACACTCACGCAGAACTGGGTTGGCTTGTAGGACAAGTCTT
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                                                                                    ACCAACACAGAGAGTGCGAGCCTGGCTTTGTTACTGAGTGGTACATCCTCGCCATTACA
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BY728212 AJ661967 UI-M-GV0-

AU199960

CB565881 CC0134655 CC0134655 CC01366545 CC0401631 BD734453 CC0401631 BD668866 BD668866 BD73422 BD73422 BB592940 AV10199960 AV101998850 CC0194124 AV101124 AV10112

Mus muscu AMGNINUC: S Mus muscu

BY727560

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us-10-626-126-6.rst

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BX643713

BX643713

BXFZp781C0629_r1 781 (synonym: hlcc4) Homo sapiens cDNA clone
DKFZp781C0629_5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="781 (synonym: hlcc4)"
/note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB;
cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 839)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Sesarch Center (DKPZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.

No s1 sequence available.

This clone (DKPZP781C0629) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lauber, J., Bahr, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.
EST (Lauber, J., Bahr, A., Mewes, H.W., Weil, B., Amid, C., et al.) Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 437; DB 5; Length 839;
Pred. No. 9.8e-120;
0; Mismatches 175; Indels
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/db_xref="taxon:9606"

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/dev_tage="adult"

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BM548665
BQ399940
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BB592940
AU199960
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BY728212
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AK081248
CB758850
BY727560
AY400784
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75.8%;
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Best Local Similarity 75.8*
Matches 569; Conservative
Contact: MIPS
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                       72.6
72.7
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CD355034 AGENCOURT
CD3556920 AMGNNUC:U
CF147822 AGENCOURT
CC431311 CH240 309
ACR4311 CH240 309
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BJ122942 BJ122942
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BJ123503
104607 MA
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BJ108530
BJ763892
BJ123503
AW654609
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           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                                                                                                                                              34239544 segs, 19032134700 residues
                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                        nucleic search, using sw model
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BQ837058
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BX851226
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995 9881:
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1. .704

Location/Qualifiers

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Location/Qualifiers

Location/Qualifiers

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                                               cDNA Library Preparation: GPCR Consortium cDNA Library Arrayed by: The i.M. A.G.B. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.B. Consortium/LLNL at: http://mage.lln.gov column: 07
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1 (bases 1 to 704)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

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Office of Cancer Genomics
Office of Cancer Institute / NIH
Bldg. 31 Rm.0407 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
TITATGICCTTAGTAGCTTTTTGCTATAATGCTAGGAAATGCTTTGGTCATTTTAGCTTTT
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853 bp mRNA linear EST 28-MAY-2003 AGENCOURT 14163426 NICHD XGC_Eyel Xenopus laevis cDNA clone IMAGE:6949081 5', mRNA sequence.
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240
                                                                                                                      261
                                                                                                                                                                                                                                                                                                          322 GCTGTATATAAGATTGTCCTCATCAGCTATGATAATACCTGTCAATCTCAAATGCTTTG 381
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHD_KGC_EPC: pCMV-SPORT6; Site_1: Not1;
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.3 kb. Constructed by Life
Technologies Note: This is a Xenopus Gene Collection
(XGC) library."
                                                                                                     202 GACTTCTTTGTGGGTGTGTGTCCATTCTTTGTACATCCCTCACACGCTGTTCGAATGG
                                                                                                                                                                  241 AAITITIGGAAGIGGAATCIGCAIGITTITIGGCICATIACTGACIATCITITIGGGAAGCA
                                                                                                                                                                                                                 262 GATTTTGGAAAGGAAATCTGTGTATTTTGGCTCACTACTGACTATCTGTTATGTACGCA
                                                                                                                                                                                                                                                             CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Phttp://image.llnl.gov
Plate: LLAM14564 row: f column: 24
High quality sequence stop: 707.
                                                                         181 GACTICTICGIGGGIGICAICICCATICCICIGIACATCCCICACACGCTGTTTAACIGG
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1 (bases 1 to 853)

NIH-MGC htp://mgc.nci.nih.gov/.

National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Genomics

National Cancer Manuel MD 20892

Email: cgapbs-remail.nih.gov

Tissue Procurement:
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59.3%; Pred. No. 3.7e-28;
tive 0; Mismatches 165; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          382 TCTTATGGAACGCAAAAACGGGGGCCTGAAGA 415
                                                                                                                                                                                                                                                                                                                                                           361 CGTTATAGAGCACAGCACACTGGCATCCTGAAAA 394
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/mol_type="mRNA"
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Matches 245; Conservative
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AGENCOURT 30842625 NIH MGC 146 Homo sapiens cDNA clone
IMAGE:7389774 5', mRNA sequence.
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a. Note: this is a NIH_MGC_Library."
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/lab_host="NH10B (T1-phage-resistant)"
/clone_lib="NH10B (T1-phage-resistant)"
/clone_lib="WH1 MGC 146"
/note="Wector: pcDNA31; Site 1: multiple; Site 2:
multiple, ORF's were PCR-amplified (from IMAGE Clones or
from commercially available cDNA libraries) and cloned by
the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)
into pcDNA31. For specific information or cloning sites
(which vary by clone), please refer to the Guthrie
website, using the Guthrie ID given in the file
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo. I (basea 1 to 721)

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10AO7 Bethesda, MD 20892

Email: cgapbs.r@mail.nih.gov
Tissue Procurement: Guthrie CDNA Resource Center
                                                 22 ATGCCAGATACTAATAGCACAATCAATTTATCACTAAGCACTCGTGTTACTTTAGCATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTAATGTCCCTGCTTGCTTTTGCTATAACGATAGGCAATGCTGTGGTCATTTTAGCCTTT
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High quality sequence start: 2
High quality sequence stop: 328.

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/db_xref="taxon:9606"
/clone="IMAGE:7389774"
                                                                                                                                                                                                                                                                                                                                                         C0959034.1 GI:51323616
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Matches 306;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
I (bases 1 to 732)
RS NIH-MGC http://mgc.nci.nih.gov/.
INIH-MGC http://mgc.nci.nih.gov/.
IAL Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genemics
National Cancer Institute of NIH
Bldg 31 Rm10A07 Bethesda, MD 20892
Email: cgapbe-romail.nih.gov
Tissue Procurement: GPCR Consortium
CDNA Library Preparation: GPCR Consortium
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
Clond distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBIO2 row: b column: 06
High quality sequence stop: 610.
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GACCGGCCGTTGGACCTTCGGCCGGGGCCTCTGCAAGCTGTGGCTGGTGGTAGACTACCT 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  348 TTCAAACGCTGTGCGTTATAGAGCACACCACTGGCATCCTGAAAATTGTTGCTCAAAT 407
                                                                                                                                                                                                                                                                                                                                                                                    526 CACTCGAGCTGTCTCCTACAGGCCCAGCAGGGGGACACGAGACGGGCCGTTCGGAAGAT
                                                                                                                                                                      GTTTAAC---TGGAATTTTTGGAAGTGGAATCTGCATGTTTTGGCTCATTACTGACTATCT
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Pred. No. 4.3e-27;
0; Mismatches 191;
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|mol_type="mRNA"
|db_xref="taxon:9606"
|clone="IMAGE:691899"
|tissue_type="mixed"
|lab_host="DH108"
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Best Local Similarity 57.0
Matches 257; Conservative
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VERSION
KEYWORDS
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ORGANISM
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DEFINITION
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           geredeciriogrados de actual de actua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 GGCTATTTCTGACTTCTTCGTGGGTGTCATCTCCATTCCTCTGTACATCCCTCACACGCT 230
                                                                                                         GICATITIAGCCITIGIAGCAGACAGAAACCITAGACATCGAAGTAATTATTITITCTT 165
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                                                                                                                                                                                                                                                                                                                       AATTIGGCIAITICIGACTICITCGIGGGIGTCAICICCATICCICIGIACAICCCICAC 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATCTGCTCTGCACCTCGTCCGTGTTCAACATCGTGCTCATCAGCTACGACAGGTTCATC 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCAGTTTCAAAACGCTGTGCGTTATAGAGCACAGCACACTGGCATCCTGAAAATTGTTGCT 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTGTGACCCGGGCTGTCAGTTACCGAGCTCAGCAGAGTAACAGCCGGCATGCAGTCTTG 741
     GTCTTCCTGGCTGTCCTGATGGGGGTCCTCATAGTTAGCACCGTGCTGGGGAATGCCCTG 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              562 GTACTGACTGGCAGATGGAGCTTTGGCAGGAGCGTTTGCAAACTGTGGCTGGTTCTGGAT 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTGGCATTTTTAATGTCCCTGCTTGTTTGCTATAACGATAGGCAATGCTGTGGTCAT
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/db_xref="taxon:10116"
/clone="urgp1-00001-d6"
/clone_lib="urgp1 (14349)"
/note="Wector: pSPORT1; Rat GPCR library rearrayed
internal pSPORT vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      742 AAAATGACCATGGTGGGATCTTGGCCTTTCTCCTATATGGACCAGCCATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAAATGGTGGCTGTTTGGATACTGGCTTTCTTGGTCAATGGCCCAATGATTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 131; DB 6; Length 67
Pred. No. 1.4e-27;
0; Mismatches 170; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Rattus norvegicus"
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Amgen EST Program.
Amgen Rat EST Program
Unpublished (2003)
Contact: Dan Fitzpatrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CB556920.1 GI:29496320
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ilarity 58.7%;
Conservative
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AUTHORS
TITLE
JOURNAL
COMMENT
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AL848045
AL848045 XGC-egg Xenopus tropicalis cDNA clone TEgg022i22 5', mRNA
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cDNA was oligo dT primed from 5ug of poly A+ RNA from egg.

ECORI-NotI cut cDNA was then ligated into pCS107 with ECORI at the 3' end and NotI at the 3' end.

Vector: pCS107; Site 1: ECORI; Site_2: NotI

Host: Escherichia coli XLI-blue.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          380 GCTCACTACTGACTATCTTTTGTGTACAGCATCTGTGTATAACATCGTACTCAGCTT 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENKATYOLE, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae, Kenopodinae, Kenopodinae, Silurana.

1 (bases 1 to 643)

Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J. Sanger Xenopus tropicalis EST project 2001 (11_2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     320 TTTATTCATCCCTCACAGCTCTTCAACTGGGAGTTTGAAATAACATTTGTGTCTTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210 TCTGTACATCCCTCACACGCTGTTTAACTGGAATTTTGGAAGTGGAATCTGCATGTTTTG
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Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SQUENCE ID: TEGG022122.plkSP6
Sequencing priner: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
                                                                                                                                                                                                                                                                                                                                                   /cell_type="Blood"
/clone_lib="CHORI-240"
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: Mbo
Hereford bull il Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On Sep 15, 2002 this sequence version replaced gi:22868310.
Contact: Taylor R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 684;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 115.6; DB 9;
Pred. No. 6e-23;
0; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus tropicalis (western clawed frog)
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                                                                                                                                      /organism="Bos taurus"
/mol type="genomic DNA"
/strain="breed: Hereford"
/db_xref="texon:9913"
/clone="CH240_309C10"
                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL848045.2 GI:38559584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 70.6%;
Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                         /sex="Male"
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Seq primer: T7
Class: BAC ends.
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AL848045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC#61311 684 bp DNA linear GSS 16-JUN-2003 CH240 309C10.T7 CHORI-240 Bos taurus genomic clone CH240_309C10, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The British Columbia Cancer Agency Genome Science Centre 600 W 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6 follow 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6 Fax: 604-877-6036 Email: rholt@bcgsc.ca Email: rholt@bcgsc.ca Clones are derived from the bovine BAC library CHORI-240 (http://www.chori.org/bacpac/bovine240.htm). For BAC library cavailability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (http://www.chori.org/bacpac/ordering_information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (1BBMC) by CSIRO Livestock Industries, Australia and the Blartish Columbia Genome Sciences Centre, Canada.

Plate: 309 row: C column: 10
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1 (Dass 1 to 684)

Holt, R., Stott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L.,

Half, R., Stott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L.,

Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A.,

Mathewson, C., Wye, N., Masson, A., Brown-John, M., Jones, S.,

Schein, J., Marram, de Jong, P., McMilliam, S., Barris, W.,

Dalrymple, B.P. and Tellam, R.

Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398

Other GSSs: CH440

Contact: Rob Holt
                                     TGGCATTTTTAATGTCCCTGCTTGCTTTTGCTATAACGATAGGCAATGCTGTGGTCATTT 112
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                                                                                                                                                                                                                                                                                                                     CTATTTCTGACTTCTTCGTGGGTGTCATCTCCATTCCTCTGTACATCCCTCACACGCTG- 231
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
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A99 bp mRNA linear EST 12-DEC-2000 UI-R-B00-agr-c-06-0-UI.rl UI-R-B00 Rattus norvegicus cDNA clone BP567596
                                                                                                                                                                                                                      /tisaue_type="embryonic stem cells, cell lines H1, H7, and
H9"
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 8.0%; Score 93.8; DB 7; Length 7
Best Local Similarity 53.9%; Pred. No. 2.3e-16;
Matches 241; Conservative 0; Mismatches 197; Indels
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                                                                                                                                organism="Homo sapiens"
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      rbrandenberger@geron.com
Length: 716 Std Brror:
Location/Qualifiers
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                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                       /clone lib="GRN ES"
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      Email:
Insert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCACAGAAAGGAATGAAAAATGCAGTGTTAAAAATGCTTATTGTTTGGGTGGCAGCC 322
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I (basea 1 to 716)

I (basea 1 to 716)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGTGGAATCTGCATGTTTTGGCTCATTACTGACTATCTTTTGTGCACAGCATCCGTCTAC 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGTATTGTCCTCATTAGCTACGATCGATACCAGTCAGTTTCAAACGCTGTGCGTTATAGA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCACAGCACACTGGCATCCTGAAATTGTTGCTCAAATGGTGGCTGTTTGGATACTGGCT 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TICITGGICAATGGCCCAATGATTCTGGCTTCGGA-----TICITGGAAGAACAGCACC 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTCTTCTCTATGGCCCAGCCATCATCACCTGGGAATACATTGCAAGAACTACTATCTTA 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      383 CCAGAAGGGGAATGTTATGTAGAATTCTACTACAACTGGTATTTTCTGATGATAGCTTCC 442
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                                                                                                                                                                                      /note="Vector: pc3107; Site_1: EcoR1; Site_2: Not1; cDNA was oligo dT primed from 5ug of poly A+ RNA from egg. EcoR1-Not1 cut cDNA was then ligated into pc3107 with EcoR1 at the 5' end and Not1 at the 3' end"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGTGTCATCTCCATTCCTCTGTACATCCCTCACACGCTGTTT---AACTGGAATTTTGGA
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                                                                                                                                                                                                                                                                                                                                                                                 Length 643;
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Pred. No. 5.4e-17;
0; Mismatches 182; Indels
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230 Constitution Drive, Menlo Park, CA 94025, USA
721 650 473 7760
/mol_type="mRNA"
/db xref="taxon:8364"
/clone="TEGQ02122"
/dev stage="egg"
/lab_host="Escherichia coli XL1-blue"
                                                                                                                                                          /clone_lib="XGC-egg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17000424504731 GRN_ES Homo
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Best Local Similarity 55.1%;
Matches 234; Conservative
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                                                                                                                                                                                                                                                                                                      /dione="UI-R-B00-agr-c-06-0-UI"
/dac grage="adult"
/lab_host="bH10B (Life Technologies)"
/dlone lib="UI-R-B00"
/dlone lib="UI-R-B00"
/dlone lib="UI-R-B00"
/dlone lib="UI-R-B00"
/dlone lib="UI-R-B00"
/dlote="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker: Site l: Not I; Site 2: Eco RI; The library
(UI-R-B00) is a subtracted library derived from a mixture
of the following tissues: thalamus, cerebellum,
hypothalamus, medulla, pons, midbrain, cerebral cortex,
corpus striatum and hippocampus. For a detailed
description of the library from which this clone was
derived, please visit our web site at
described in (Bonaldo, Lennon and Soares, Genome Research
Coordinated Laboratory for Computational Genomics
University of Iowa
1915 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
1915 319 315 8256
Fax: 319 315 9565
Email: bento-soarse@uiowa.edu
CDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
Liblu (info@image.llnl.gov).* IMAGE ID= 1796445
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                                                                                                                                                                                                                                     /organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
                                                                                                                                                                                                                                                                                             db_xref="taxon:10116"
                                                                                                                                                                                                   .ocation/Qualifiers
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Matches 234; Conserv
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RESULT 11 CNS03296/c

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921 bp DNA linear GSS 01-SEP-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 206D09 of library G from Tetraodon nigroviridis, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr. The b: www.genoscope.cns.fr. as is sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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                                                                                                                                                                                                                                                                                          Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetradontoidea; Tetraodontidae; Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bouneau, L., Fisher, C.,
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/note="Genoscope sequence ID : COAG206CB05LP1~end : T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C. Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of freshwater puffertish Tetraodon nigroviridis Genome Res. 10 (7), 939-949 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
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59.4%; Pred. No. 6e-15;
ve 0; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Tetraodon nigroviridis"
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/db_xref="taxon:99883"
                                                                                                                                                                                                GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="206D09"
                                                                                                                                      AL224547
AL224547.1 GI:7883412
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Conservative
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, P.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Butcow, K.H., Scheefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsteh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.M. B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwant, P.J.,
McKernan, K.J., Malle, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Vilalon, D.K., Mizny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Gchnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and muital analysis of more than 15,000 full-length
human and mouse cDNA sequences

IL Proc. Natl. Acad. Sci. U.S.A., 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue_type="Mammary tumor. WAP-TGF alpha model. 7 months
                                                                                          HTC 25-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H. Garcia, A.M., Lu, X., Hulyk, S.W., Louleeged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 1136)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (19-DEC-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 37 Row: a Column: 16 Series: IRAK Plate: 17 Row: a Column: 16 Edentity but not passed the following selection criteria: Similarity but not identity to protean This clone has the following problem: frame shifted.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Trissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                    Mus musculus cholinergic receptor, muscarinic 2, cardiac, mRNA (cDNA clone IMAGE:4036375), containing frame-shift errors.
                                                                                              linear
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                                                                                              mRNA
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/#strain="mix PWB/N, CS7BL/6J"
/db_xref="texon:10090"
/clone="IMAGE:4036375"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
                                                                                              1136 bp
                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
                                                                                                                                                                                                           BC019470.1 GI:18044479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing Center
Center code: BCM-HGSC
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TITLE
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                            RESULT 13
BC019470
                                                                                                                                                                                  ACCESSION
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REFERENCE
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KEYWORDS
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COMMENT
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                                                                                                                                                                                                                                                                       SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:6311932"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/clone | MGC 129"
/note="Organ: OlfacTory epithelium; Vector: pCMV-SPORT6.1;
Site 1: BCORV; Site 2: Not1; Cloned unidirectionally.
Primer: Oligo dT. Average insert size 2:2 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NIH_MGC
                                                                                                       1046 bp mRNA linear EST 21-AUG-2002
AGENCOURT 8863943 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6311932
BQ950659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    438 TAGGTGCCTTCTGCATCCCATTGTATGTACCCTATGTGCTGACCGGCCGTTGGACCTTTG 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        centectigerenatiogecerecentectionerisogaenacerorecegeoceaecteca 737
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NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbe.remail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.

CDNA Library Preparation: ResGen, Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC.clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:

http://image.llnl.gov

Rolumn: 05

High quality sequence stop: 640.
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352 CCCAAAAGACAGTCGGTTCAGCCTCAGATCGAAGTCCAGTCGTGTTAA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.2%; Score 84.2; DB 5; Length 1 ilarity 56.5%; Pred. No. 2e-13; Conservative 0; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
                                                                                                                                                                                                                                                                       BQ950659.1 GI:22366137
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                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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Matches 177;
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TITLE
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COMMENT
                                                                                       RESULT 12
BQ950659
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KEYWORDS
SOURCE
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This clone will not be made available due to an unidentified
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S McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,

Bowcater, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,

Bowcater, J., Clifton, M., Ritter, E., Bennett, J., Franklin, C.,

Tagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,

Underwood, K., Steptoo, M., Allen, M., Person, B., Swaller, T.,

Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,

McCann, R., Waterston, R. and Wilson, R.,

The Washington Univ. Nematode EST Project, 1999

Contact: McCarter JP

The Washington Univ. Nematode EST Project, 1999

Washington University School of Medicine

Washington University School of Medicine

Washington University School of Medicine
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                                                                                                                                                                                                                   CITGCITITGCIAIAACGAIAGGCAAIGCIGIGGICAITITAGCCITIGIAGCAGACAGA 132
                                                                                                                                                                                                                                                                                                    133 AACCTTAGACATCGAAGTAATTATTTTTTTTTTAATTTGGCTATTTCTGACTTCTTGGTG 192
                                                                                                                                                                                                                                                                                                                                                                                       GGTGTCATCTCCATTCCTCTGTACATCCCTCACACGCTGTTT---AACTGGAATTTTGGA 249
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Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.
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                                                                                                                              Length 1136;
                                                                                                                           7.0%; Score 82.2; DB 3; Length 1
56.3%; Pred. No. 8.3e-13;
ive 0; Mismatches 133; Indels
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old, gross tissue."
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/db_xref="taxon:6305"
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Fax: 314 286 1810
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Meloidogyne hapla
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Enkaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Enkaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchida; Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.

Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.

Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.

Mocarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylle, T., Dante, M., Mitter, E., Bannett, J., Franklin, C., Tagareishvill, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., McGann, R., Waterston, R. and Wilson, T., Jackson, Y., Cardenas, M., McGann, R., Waterston, R. and Wilson, R. The Washington Univ. Nematode EST Project, 1999

Lontact: McCarter JP

The Washington Univ. Nematode EST Project, 1999

Washington University School of Medicine
/lab_nost="DHIOB"
/clome lib="Meloidoyne hapla J2 pAMP1 v1"
/clome lib="Meloidoyne hapla J2 pAMP1 v1"
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The library was constructed by Claire Murphy and Dr. James
McCarter at Washington University, St. Louis. The CDNA was
made by using Dynabead oligo-dT priming (Dynal). PCR based
library using a modified protocol from the SMART PCR cDNA
Synthesis Kit from Clontech. Directionally cloned into the
Williamson of pAMP1. J2 were provided by Dr. Valerie
Williamson of the University of California at Davis
(vmwilliamson@ucdavis.edu)."
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rf47c11.yl Meloidogyne hapla J2 pAMP1 v1 Meloidogyne hapla cDNA 5'
similar to TR:Q9XW31 Q9XW31 Y40H4A.1 PROTEIN. [1] ;, mRNA sequence.
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Far: 314 286 1810
Email: est@watson.wustl.edu
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56.0%; Pred. No. 3.3e-12;
tive 0; Mismatches 132;
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nes 172; Conserv
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The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dynal). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pAMP1. J2 were provided by Dr. Valerie Williamson@ucdavis.edu)."
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6.6%; Score 78.2; DB 5; Length 410;
Best Local Similarity 55.7%; Pred. No. 9.3e-12;
Matches 171; Conservative 0; Mismatches 133; Indels 3; Gaps
microbial contamination of the source material.
Seg primer: -40RP from Gibco.
Location/Qualifiers
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Job time : 3701 secs
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      GenCore
Copyright (c) 1993
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Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000

0B 0B 0B

Minimum Maximum M

Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Post-processing:

Geneseq 16Dec04:*

Database

geneeqp19808:* geneeqp19908:* geneeqp2000s:* geneeqp2001s:* geneeqp2003s:* geneeqp2003bs:* geneeqp2003bs:*

2105692 seqs, 386760381 residues

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Histamine H4 receptor; rat; antiasthmatic; antiallergenic; antiinflammatory; cardiant; circulatory; antidiabetic; laxative; AAM50566 standard; protein; 391 AA (ORTH ) ORTHO-MCNEIL PHARM INC 22-FEB-2001; 2001WO-US005914 31-MAY-2000; 2000US-0208260P (first entry) histamine H4 receptor. antiinflammatory; cardidiagnosis; gene therapy Liu WO200192485-A1. Rattus rattus. Lovenberg T, 18-MAR-2002 06-DEC-2001 AAM50566; Rat RESULT 1 

> Mouse Mouse AAM50565 ADO29497 AAB02831 В Length Query Match Score

Result

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Human G p Human orp Human G p Human G p Human G p Human G p Human his Human G p Human his Human G p end end hum his GPC GPC his GPC Human Human Human Novel Aay71297 Aab62445 Aab73627 Aam53050 Abb798629 Abb788629 Abg71986 Abg71960 Abg71960 Abg71265 Abg81727 Abg81727 Abg88760 Adg88760 Adg88760 Adg88776 AAY71297 AAB62445 AAG64477 AAB73622 AAM53050 ABP98629 ABB78276 AAMS0564 AAG66023 AAU74906 ABG71960 ABU92265 ABP81727 AAE36417 ADG98760 ADO05720 ADO29496 ADP20168 ADG86375 ADJ88376 ADJ26923 40000000000000 1442 1442 1442 1443 14603.5 14603.5 14603.5 14603.5 14603.5 14603.5 14603.5 14603.5 14603.5 14603.5 14603.5 14603.5 222210987654321098765432 Š.

New mammalian histamine H4 receptor proteins and polynucleotides encoding the proteins, useful in gene therapy for treating diseases where it is beneficial to elevate mammalian histamine H4 receptor activity.

WPI; 2002-114339/15.

N-PSDB; AAI70982

Claim 13; Fig 6A; 92pp; English.

The present sequence is that of a rat histamine receptor of the H4 subtype, as predicted from a cDNA clone isolated from a spleen cDNA library. The invention provides mammalian (human, mouse, rat and guinea pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and polypeptides (see AAM50564-67). The nucleic acids have been expressed in recombinant host calls that produce active recombinant protein. The pharmacology of known histamine ligands is demonstrated. Mammalian histamine H4 receptor may be used in gene therapy for the treatment of histamine H4 receptor activity. Recombinant protein is useful for identifying modulators of the histamine H4 receptor. Such modulators may be useful

Human

Human G p Human G p Human G p Human GPR Human H4 Human mAC
Human G p
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A human his
Human his
Human his Guinea pi Human H4 Human H4 Monkey hi Monkey hi Adms1410
Adg 8416
Adg 8416
Adg 8416
Adg 8415
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Abr 4364
Adg 7411
Adg 7411 AAB36416 ADG86522 AAB50567 AAB3068 AAB36415 AAB3668 ABP57426 ABP57426 AAG6322 AAG6322 AAG6322 AAG6323 AAG6323 AAG6323 AAG6323 AAG6330 AAG6330 AAG6330 

ALIGNMENTS

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                                                                                                                                                                                                                                               DFFVGVISIPLYIPHTLFNWNFGSGICMFWLITDYLLCTASVYSIVLISYDRYQSVSNAV 120
                                                                                                                                                                                                                                                                                                       RYRAQHTGILKIVAQMVAVWILAPLVNGPMILASDSWKNSTNTEECEPGFVTEWYILAIT 180
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for diagnosing, treating or preventing asthma, allergy, inflammation, cardiovascular and cerebrovascular disorders, non-insulin dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders the neuroendocrine system, stress and spasticity
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                                                                                                                                       Gaps
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                                                                                                         Length 391;
                                                                                                                                     1; Indels
                                                                                                       Score 2034; DB 5;
Pred. No. 2.3e-203;
0; Mismatches 1;
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                                                                                                    Query Match
Best Local Similarity 99.7%;
Matches 390; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse histamine H4 receptor.
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diagnosis; gene therapy.
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                                                                         Sequence 391
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The present sequence is that of a mouse histamine receptor of the H4 subtype, as predicted from a cDNA clone isolated from a spleen cDNA library. The invention provides mammalian (human, mouse, rat and guinea pig) histamine H4 receptor nucleic acid molecules (see AA170980-83) and polypeptides (see AAN50564-67). The nucleic acids have been expressed in recombinant host cells that produce active recombinant protein. The pharmacology of known histamine ligands is demonstrated. Mammalian histamine H4 receptor may be used in gene therapy for the treatment of diseases where it is beneficial to elevate mammalian histamine H4 receptor activity. Recombinant protein is useful for identifying modulators of the histamine H4 receptor. Such modulators may be useful for diagnosing, treating or preventing asthma, allergy, inflammation, cardiovascular and carebrovascular disorders, non-insulin dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of the neuroendocrine system, stress and spasticity
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beneficial to elevate mammalian histamine H4 receptor activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 391;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
85.2%; Score 1742; DB 5;
Best Local Similarity 84.9%; Pred. No. 7.5e-173;
Matches 332; Conservative 17; Mismatches 42;
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                                         5B; 92pp; English
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                                     Claim 13; Fig
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The invention relates to human and mouse G protein-coupled receptors

(GPCRS) and nucleic acids encoding them. The invention also relates to

sequences at least 90% identical to the GPCR proteins and nucleic acids

of the invention; methods of treating, preventing or diagnosing diseases

compounds useful in the treatment of GPCR related diseases, at transgenic

compounds useful in the treatment of GPCR related diseases, at transgenic

compounds useful in the treatment of GPCR related diseases, at transgenic

compounds useful in the treatment of GPCR related diseases, at transgenic

computes comprising a GPCR gene of the invention; a mouse comprising a

mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived

comprising a dPCR mucle; kits comprising several mice, each of which has

comprising a dPCR mucleic acid. The GPCR mucleic acids and proteins may

be used in the diagnosis, treatment or prevention of a wide variety of

diseases including neurological disorders (e.g., Alzheimer's disease,

comprising a GPCR mucleic acid. The GPCR mucleic acids and proteins may

be used in the diagnosis, treatment or prevention of a wide variety of

disorders of the adrenal gland; disorders (e.g., Alzheimer's disease,

cell of safewarded; in functional disorders (e.g., Alzheimer's disease,

compounding neuropathy, Parxheson's disease or stratable bowel

compound a disease, diarrhoea, food poisoning or intratable bowel

compounded infarction); muscular disorders (e.g., outclammen disorders (e.g.,

AIDS); bone and joint disorders (e.g., outclammen disorders (e.g.,

cobseity, enzyme deficiency-related diseases or vitamin deficiency-related

constitution disperse of the kidney liver lund heart of the colon or intestine

constitution of the kidney of the kidney or vitamin deficiency-related

constitution disperse of the kidney or vitamin deficiency-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diseases); and disorders of the kidney, liver, lung, breast, ovary, uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and thyroid (e.g., cancers). The present sequence represents a GPCR of the invention. Note: The full sequence data for this parent did not form part of the printed specification; those sequences not shown were obtained in
thymus disorder; thyroid disorder; antiparkinsonian; antimanic; cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic; CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic; virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic; dermatological; antiulcer; antithyroid; antiallergic; anorectic; immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina
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Zeng H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gragerov A, Houman.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pavlova MN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pectoris, Parkinson's disease.
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Mcilwain KL, Pav
                                                                                                                                                                                                                                                                                                                                                                                                   09-SEP-2002; 2002US-0409303P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-390329/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PRIM-) PRIMAL INC.
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                                                                                                                                                    murine; receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaitanaris GA,
                                                                                                                                                                                                        Mus musculus.
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                                                                                                                        240
                                                                                                                                   181 MLLEFILLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSSASGHLHRAGVACRTSN 240
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                                                                                                                                                                                                                                                                                                                                                                                                                         Human, G protein coupled receptor, GPCR; transmembrane receptor,
identification, agonist, screening, therapeutic, pharmaceutical, mutant.
DFLVGLISIPLYIPHVLFNWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAV
                                                                                      121 SYRAQHTGIMKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPGFVTEWYLLTT
                                                                                                                        181 AFLEFLLPVSLVVYFSVQIYWSLWKRGSLSRCPSHAGFIATSSRGTGHSRRTGLACRTSL
                                                                                                                                                                              241 PGLKESAASRHSESPRRKSSILVSLRTHMNSSITAFKVGSFWRSESAALRQREYAELLRG
                                  DFFVGVISIPLYIPHTLFNWNPGSGICMFWLITDYLLCTASVYSIVLISYDRYQSVSNAV
                                                                                                                                                                   PGLKEPAASLHSESPRGKSSLLVSLRTHMSGSIIAFKVGSFCRSESPVLHQREHVELLRG
                                                                                                                                                                                                              RKLARSLAVLLSAFAICWAPYCLFTIVLSTYRRGERPKSIWYSIAFWLQWFNSLINPFLY
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99US-0120416P.
99US-0123944P.
99US-0123946P.
99US-0123946P.
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99US-0136430P.
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12-MAR-1999;
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28-MAY-1999;
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Query Match 85.2%; Score 1742; DB 8; Best Local Similarity 84.9%; Pred. No. 7.5e-173; Matches 332; Conservative 17; Mismatches 42;

Length 391; Indels

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02-NOV-2000 (first entry)
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                                                                                                                                                                                                                         The present invention describes transmembrane receptors, preferably human g protein coupled receptors (GPCR), for which the endogenous ligand is unknown (orphan GPCR receptors). More specifically the present invention relates to non-endogenous, constitutively activated versions of a human GPCR. These non-endogenous human GPCRs can be useful for the direct identification of candidate compounds as receptors agonists, inverse agonists or partial agonists for use as pharmaceutical agents. AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 SYRIQHTGVLKIVILMVAVWVLAFLVNGPMILVSESWKDBGS--ECEPGFFSEWYILAIT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPLEFVIPVILVAYFNMNIYWSLWKEDHLSRCQSHPGLTAVSSNICGHSFRGRLSSRRSL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 SASTEVPASFHSERQRKKSSLMFSSRTKMNSNTIASKMGSFSQSDSVALHQREHVELLRA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DFFVGVISIPLYIPHTLFNWNPGSGICMFWLITDYLLCTASVYSIVLISYDRYQSVSNAV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RYRAQHTGILKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTEECEPGFVTEWYILAIT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AFLEFLLPVSLVVYFSVQIYWSLWKRGSLSRCPSHAGFIATSSRGTGHSRRTGLACRTSL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 PGLKEPAASLHSESPRGKSSLLVSLRTHMSGSIIAFKVGSFCRSESPVLHQREHVELLRG 300
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                                                                                                                                                                          Non-endogenous, human G protein-coupled receptors for screening receptor, inverse or partial agonists useful as therapeutic agents.
                                                                                                                                                                                                                                                                                                                                                                                                       1 MSESNGTDVLPLTAQVPLAFLMSLLAFAITIGNAVVILAFVADRNLRHRSNYFFLNLAIS
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                                                                                                               Dang HT;
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                                                                                                                                                                                                                                                                                                                                                              pred. No. 1.7e-137;
40; Mismatches 78; Indels
                                                                                                               Chen R,
                                                                                                                        Lowitz K, White C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 PLCHRRPOKAFWKILCVTKOPAPSO-TOSVSS 391
                                                                                                               Chalmers DT,
                                                                                                                                                                                                                                                                                                                                                     Query Match 68.6%; Score 1403.5; Best Local Similarity 69.1%; Pred. No. 1.7e Matches 271; Conservative 40; Mismatches
                                                                                                                                                                                                         Example 1, Page 89-90; 187pp; English.
99US-0156653P.
99US-0157281P.
99US-0157281P.
99US-0157283P.
99US-0157294P.
99US-00416760.
                                                                                                               Lehmann-Bruinsma K,
                                                                                                                        Liaw CW, Lin I,
                                                                                          (AREN-) ARENA PHARM INC.
                                                                                                                                            WPI; 2000-317986/27.
N-PSDB; AAA46023.
                                                                                                                                                                                                                                                                                                                                  Sequence 390 AA;
                            01-OCT-1999;
01-OCT-1999;
01-OCT-1999;
12-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present amino acid sequence is the hRUP7, an endogenous human orphan G protein-coupled receptor (GPCR). The full length hRUP7 cDNA was cloned by RT-PCR using human peripheral leucocyte cDNA as template. The orphan GPCR of the invention, like all GPCRs has seven transmembrane aliphan helices with an extracellular N-terminus and an intracellular C-terminus. However, no endogenous ligands has yet been identified for the proteins of the invention. The orphan GPCRs may be used in the identification of antagonists for use as pharmaceutical agents. The proteins may also be used in the study of GPCR-mediated signalling cascades, and to elucidate their precise role in normal and diseased human conditions. Nucleic acid expression analysis to provide information about their function in healthy and pathological states
                                                   Human; orphan G protein-coupled receptor; GPCR; hRUP7; drug screening;
transmembrane receptor; signal cascade.
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69.1%; Pred. No. 1.7e-137;
tive 40; Mismatches 78; Indels 3;
Human orphan G protein-coupled receptor hRUP7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 26; Page 60-61; 102pp; English.
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9905-0121852P-
9905-0123949P-
9905-0136437P-
9905-0136437P-
9905-0136567P-
9905-0137127P-
9905-0137127P-
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9905-015655P-
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99US-00416760.
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1 MSESNGTDVLPLTAQVPLAFLMSLLAFAITIGNAVVILAFVADRNLRHRSNYFFLNLAIS 60

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AAY71297 standard; protein; 390 AA

AAY71297

RESULT 5
AAY71297
ID AAY7
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AC AAY7
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Query Match 68.6%
Best Local Similarity 69.1%
Matches 271; Conservative
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                                                                                                                                            180
                                                                                                                                                                                                                                                                238
                                                                                                                                                                                                                                                                                                                            239 SASTEVPASFHSERQRRKSSLMFSSRTKMNSNTIASKMGSFSQSDSVALHQREHVELLRA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G-protein coupled receptor; GPCR; PFI-013; antiallergic; antiasthmatic; antiinflammatory; vasotropic; antidiabetic; anorectic; cytostatic; human; osteopathic; neuroprotective; nootropic; dermatological; gynecological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New G-protein coupled receptor-like polypeptide, polynucleotide for screening drug candidates for treating diseases associated with signal transduction e.g. allergic, inflammatory, pulmonary, neoplastic diseases.
                        9
DFFVGVISIPLYIPHTLFNWNPGSGICMFWLITDYLLCTASVYSIVLISYDRYQSVSNAV
                                                                                                                                          RYRAQHTGILKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTEECEPGFVTEWYILAIT
                                                                                                                                                                                                                        AFLEFLLPVSLVVYFSVQIYWSLWKRGSLSRCPSHAGFIATSSRGTGHSRRTGLACRTSL
                                                                                                                                                                                                                                                              SFLEFVIPVILVAYFNWNIYWSLWKRDHLSRCQSHPGLTAVSSNICGHSFRGRLSSRRSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human GPCR-like polypeptide, PFI-013.
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(PFIZ ) PFIZER INC.
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intrinsic asthma, vasculitic granulomatous disease, interstitial and other pulmonary disease, including chronic obstructive pulmonary disease (COPD), infectious, inflammatory disease, such as inflammatory bowel disease and neoplastic and myeloproliferative diseases. They are also useful for treating obesity, diabetes, metabolic, neurological diseases, sychotherapeutics, urogenital disease, reproduction and sexual medicine, inflammation, cancer, tissue repair, dermatology, photoagaing, skin pigmentation, cancer, tissue repair, dermatology, photoagaing, skin pigmentation, osteoporosis, cardiovascular, gastrointestinal diseases, allergy and respiratory disease, sensory organ disorders, aleap disorders and hair loss. The PFI-013 protein and nucleic acid are useful in the diagnosis and treatment of the above conditions and also for screening transduction. The antibodies are also useful for enrichment of cosinophils from mammalian, especially human blood and for detecting the protein in biological samples
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASVYNIVLISYDRYLSVSNAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 SYRTQHTGVLKIVTLMVAVWVLAFLVNGPMILVSESWKDEGS--ECEPGFFSEWYLLAIT
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; Pred. No. 1.7e-137;
40; Mismatches 78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          390
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69.1%;
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The present sequence is that of the human G protein-coupled receptor protein BG26, which shows significant homology with histamine H3, with activity of binding to histamine and capable of changing intracellular CAMP concentration in response to its stimulus. The protein is applicable as a tool in screening ligands or drug candidates for regulating signal transduction from such protein and treating diseases associated with its
                                                                                                                                             G protein-coupled receptor protein BG26, with activity of binding to histamine and capable of changing intracellular CAMP concentration in response to its stimulus, applicable as tool in screening ligands or drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RYRAQHTGILKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTEBCEPGFVTBMYILAIT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                        Length 390;
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; Pred. No. 1.7e-137;
40; Mismatches 78;
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                                                                Ohta M;
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                                                                                                                                                                                                                            Claim 1, Page 41-44; 50pp; Japanese.
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                                                                 Tanaka
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 99JP-00361687
                            (BANY ) BANYU PHARM CO LID
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                                                                Itadani H, Nakamura
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                                                                                              WPI; 2001-441675/47
                                                                                                               N-PSDB; AAH47911.
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 390 AA;
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acute heart failure; hypotension; hypertension; angina pectoris; myocardial infarction; stroke; ulcer; migraine; vomiting; psychotic disorder; neurological disorder; anxiety; schizophrenia; manic depression; bipolar disorder; depression; dellirium; dementia; severe mental retardation; dyskinesia; Parkinson's disease; Huntington's disease; Huntington's disease; Gilles de la Tourette's syndrome; lymphocyte; macrophage; eosinophil; neutrophil; function modulation; autoimmune disorder; pulmonary disorder; gene therapy; vaccine; drug screening; signal transduction; transgenic animal; drug discovery.

Homo sapiens.

O200133221-A1

10-MAY-2001.

26-OCT-2000; 2000WO-US029461

02-NOV-1999; 99US-00431898 03-FEB-2000; 2000US-00497790.

(SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.

Aubart KM, Bergsma DJ, Fitzgerald LR, Graybill TL, Li X; Michalovich D, Morrow DM, Zhu Y;

WPI; 2001-316464/33.

N-PSDB; AAH24007.

Novel G-protein coupled receptor polypeptide and polynucleotide for treating cancer, autoimmune, pulmonary, cardiovascular and neurological disorders and for identifying modulators useful for treating asthma.

Claim 1; Page 50-51; 54pp; English.

The invention relates to the human of protein-coupled receptor AXOR35

CAMPS-15.1, to CDNA encoding AXOR35 (AAM15006), and to AXOR35 fragments
and variants. Like all of protein-coupled receptors, AXOR35 has an an an an an an an analysis of protein-coupled receptors such the composition of a such that are compared to the composition of AXOR35 and to an AXOR35-specific antibody. AXOR35 proteins and notections and host cells comprising AXOR35 DNN, to recombinant expression of AXOR35, and to an AXOR35-specific antibody. AXOR35 proteins and nucleotides may be used to treat a wide variety of disorders and nucleotides may be used to treat a wide variety of disorders and nucleotides may be used to treat a wide variety of disorders including bacterial, fungal, protozoal and viral infections, particularly HIV-1 or HIV-2 infections, palimia; osteoporosis; asthma; allerqies; urinary retention; acute heart failure; hypotension, hypertension; angina percention, acute heart failure; hypotension, hypertension; and percention; acroers, benign prostatic hypertension; and percention; acroers, and severe mental.

CC diabetes; obesity; anoraxia; bulimia; osteoporosis; acthma; allerqies; urinary retention; acroers, benign prostatic hypertension; and percention; acroers, benign prostation; and dyskinesias, such as Parkinson's disease, multiplic and neurological disorders and sarxiety; achisophresion, depression, depression, depression, depression, depression, depression, depression, and dyskinesias, and acroers, multiplicing or promoting the unclouding as are useful as vaccines, and AXOR35 proteins, unclocides are also multiplicy or expression. Such AXOR35 proteins and antibodies are also astricularly useful for treating asthma, and inhibiting or promoting the detection of hyphocytes, macrophages, costnophis or meurophis or meurophis or asthmatic lung. AXOR35 proteins, nucleotides and antibodies are useful for diagnostic reagents, in chromosome localisation and protociders are useful for mutations in the corresponding gene. AXOR35 pr

Sequence 390 AA;

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241 PGLKEPAASLHSESPRGKSSLLVSLRTHMSGSIIAFKVGSFCRSESPVLHQREHVELLRG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; histamine receptor; receptor; inflammation; asthma; allergy; atopic dermatitis; stroke; myocardial infection; migraine; chronic obstructive pulmonary disease; COPD); rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          multiple sclerosis; İnflammatory bowel disease; psoriasis;
intracellular second messenger pathway; cellular growth rate;
sclerosis, inflammatory bowel disease and psoriasis
                                                                           68.6%; Score 14u3...,
69.1%; Pred. No. 1.7e-137;
Five 40; Mismatches 78;
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Best Local Similarity 69.13
Matches 271; Conservative
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HEDRICK J A.
LAZ T M.
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UMLAND S P.
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                                                                                                                                                                                                                                     SYRTQHTGVLKIVTLMVAVWVLAFLVNGPMILVSESWKDEGS--ECEPGFFSEWYILAIT 178
                                                                                                                        241 PGLKEPAASLHSESPRGKSSLLVSLRTHMSGSIIAFKVGSFCRSESPVLHQREHVELLRG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents the amino acid sequence of a human histamine receptor (HR) designated SP9144. The sequence was isolated by searching databases with the sequence of known G-coupled protein receptor (GCPR). The gene is used for recombinant production of HR and for preparing antibodies (Ab). These Ab are used to purify HR by immunoaffinity chromacography, in immunoassay of histamine receptor, to identify cDNA clones that express the receptor, as antagonist to block binding of histamine (for treating any histamine-associated disorder) and to histamine (for treating any histamine-associated disorder) and to protein can be used in the treatment of e.g. inflammation, asthma, allergy, atopic dermatitias, erroke, myocardial infarction, migraine, chronic obstructive pulmonary disease, rheumatoid arthritis, multiple
                                                              SFLEFVIPVILVAYFNMNIYWSLMKRDHLSRCQSHPGLTAVSSNICGHSFRGRLSSRRSL
                                        AFLEFLLPVSLVVYFSVQIYWSLWKRGSLSRCPSHAGFIATSSRGTGHSRRTGLACRTSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   leic acid encoding antigenic part of human histamine receptor for preparing antibodies, e.g. for treating-histamine related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Umland SP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Monsma FJ, Morse KL,
                                                                                                                                                                                                                                                                                                                        PLCHKRFQKAFLKIFCIKKQPLPSQHSRSVSS 390
                                                                                                                                                                                                                                                                                             PLCHRRFQKAFWKILCVTKQPAPSQ-TQSVSS 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Col 27-30; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP98629 standard; protein; 390 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laz TM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human histamine receptor SP9144.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SCHE ) SCHERING CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-442063/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      psoriasis; receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-OCT-1999;
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Ношо

Wang S;

RESULT 10
RESULT

SP;

Umland

Morse KL,

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Human, nGPCR-2067, G protein-coupled receptor; 7TM receptor;
signal transduction, mental disorder; central nervous system disease;
wetabolic disease; infection, HIV-1; path; neurological disorder;
wetabolic disease; infection, HIV-1; path; neurological disorder;
psychotic disorder; Huntington's disease; schizophrenia; migraine;
depression; anxiety; bipolar disorder; cancer; psoriasis;
M parkinson's disease; proliferative disorder; cancer; psoriasis;
hengn prostatic hypertrophy; diabetes; dyslipidaemia; obesity; anorexia;
thyroid disorder; cardiovascular disease; hypotension; hypertension;
thyroid disorder; ranal infarction; cardiomyopath; atherosciarosis;
inflammatory conditions; autoimmune disorder; renumatoid arthritis;
wormonal disorder; renal failure; anti-HIV; analgesic; cytostatic;
antidiabetic; metabolic; hypertensive; hypotensive; thrombolytic;
antiparkinsonian; tranquiliser; antidepressant; neuroprotective;
anticonvulsent; antidifammatory; antidepressant; neuroprotective;
anticonvulsent; antidiffammatory; antidepressant; neuroprotective;
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                                                                                                                                                                   61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASVYNIVLISYDRYLSVSNAV 120
                                                                                                                                                  DFFVGVISIPLYIPHTLFNWNPGSGICMFWLITDYLLCTASVYSIVLISYDRYQSVSNAV 120
                                                                                                                                                                                                                        RYRACHTGILKIVAOMVAVWILAFLVNGPMILASDSWKNSTNTEECEPGFVTEWYILAIT 180
                                                                                                                                                                                                                                             121 SYRTQHTGVLKIVTLMVAVWVLAFLVNGPMILVSESWKDEGS--ECEPGFFSEMYILAIT 178
                                                                                                                                                                                                                                                                                                                                    SFLEFVIPVILVAYFNMNIYWSLWKRDHLSRCQSHPGLTAVSSNICGHSFRGRLSSRRSL 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                              301 RKLARSLAVLLSAFAICWAPYCLFTIVLSTYRRGERPKSIWYSIAFWLQWFNSLINPFLY 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWFNSFVNPLLY 358
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                                                                          1 MSESNGTDVLPLTAQVPLAFLMSLLAFAITIGNAVVILAFVADRNLRHRSNYFFLNLAIS
                                                                                                AFLEFLLPVSLVVYPSVQIYWSLWKRGSLSRCPSHAGFIATSSRGTGHSRRTGLACRTSL
                                                                                                                                                                                                                                                                                                                                                                      241 PGLKEPAASLHSESPRGKSSLLVSLRTHMSGSIIAFKVGSFCRSESPVLHQREHVELLRG
                                           Gape
                                         3.
     DB 4; Length 390;
 68.6%; Score 1403.5; DB 4 69.1%; Pred. No. 1.7e-137; ive 40; Mismatches 78;

    41
    label= Transmembrane_domain_1

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/label= Transmembrane_domain_4
172. 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 PLCHRRFOKAFWKILCVTKQPAPSQ-TQSVSS 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human G protein-coupled receptor nGPCR-2067.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM53050 standard; protein; 390 AA
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Query Match
Best Local Similarity 69.11
Matches 271; Conservative
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This sequence represents a novel human G protein-coupled receptor (GPCR) designated nGPCR-2067. Like all GPCRs, nGPCR-2067 has 7 putative cransmembrane domains and is involved in signal transduction. The invention also relates to expression vectors and host cells comprising nucleic acids encoding nGPCR-2067, to recombinant expression of nGPCR-CC invention also relates to expression vectors and host cells comprising nucleic acids encoding nGPCR-2067, to recombinant expression of nGPCR-2067 and to modulators of nGPCR-2067 activity. nGPCR-2067 and species homologues and may also be used in genetic mapping. The invention also discloses the use of nGPCR-2067 activity nGPCR-2067 invention also discloses the use of nGPCR-2067 activity nGPCR-2067 invention also discloses the use of nGPCR-2067 activity nGPCR-2067 invention also discloses the use of nGPCR-2067 activity nGPCR-2067 invention also discloses the use of nGPCR-2067 activity nGPCR-2067 invention also discloses the use of nGPCR-2067 activity nGPCR-2067 incles or for the diagnosis of these disorders in GPCR-2067 mucleules for suppression of these disorders in nGPCR-2067 modulators may be used to treat a wide variety of modulators may be used to reat a wide variety of medical infections, particularly mental disorders, central nervous system conditions, particularly MIV-2 infections; pain; central nervous system, neurological and psychotic disorders such as Huntington's diseases, and metabolic diseases that may be treated cinclude cviral infections, particularly MIV-2 infections; pain; central cdementia, Alzheimer's disease, and Parkhimatory and psoriasis; cdementia, Alzheimer's disease, producers such as cancers, benign prostatic hypertrophy and psoriasis; concernia, thrombosis, myocardial infection, cardiowyopathies, and pervance and resource and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide, useful for identifying modulator compounds which are used for treating psoriasis, schizophrenia, diabetes, encodes the novel G protein-coupled receptor (nGPCR) polypeptide (nGPCR-2067).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 RYRAQHTGILKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTGECEPGFVTEWYILAIT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rheumatoid arthritis); hormonal disorders; and renal failure
                  305. 326
/label= Transmembrane_domain_6
342. 360
/label= Transmembrane_domain_7
label= Transmembrane_domain_5
                                                                                                                                                                                                                                                                                                                                                                   Wood LS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 31; Page 63; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                 Vogeli G,
                                                                                                                                                                                                                                                                                                                    (PHAA ) PHARMACIA & UPJOHN CO
                                                                                                                                                                                                                             08-MAY-2001; 2001WO-US014750.
                                                                                                                                                                                                                                                                       08-MAY-2000; 2000US-0203108P
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                                                                                                                                                                                15-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SFLEFVIPVILVAYFNWNIYWSLWKRDHLSRCQSHPGLTAVSSNICGHSFRGRLSSRRSL 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239 SASTEVPASFHSERQRRKSSLMFSSRTKMNSNTIASKWGSFSQSDSVALHQREHVELLRA 298
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                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a histamine receptor. The polypeptide is useful for identifying an agonist or antagonist of a mammalian histamine receptor. It is useful as an antigen to elicit the production of antibodies. The histamine receptor polypeptide and polymucloptide are useful in the treatment and management of diseases such as inflammation, asthma, allergy, atopic dermatitis, stroke, myocardial infection, migraine, chronic obstructive pulmonary disease (COPD), rheumation arthritis, multiple sclerosis, inflammatory bowel disease and psoriasis. They are also useful for modulating intracellular second messenger pathway activated through histamine receptors (cyclic-AMP, calcium, inosito) phosphate and mitogen activated protein (MAP) kinase), changes in cellular growth rate, secretion of hormones, receptor-stimulated Ca2+
                                                                                                                                                                Novel mammalian histamine receptor polypeptide useful for identifying agonist or antagonist for treating diseases such as inflammation, asthma, stroke, migraine, rheumatoid arthritis, multiple sclerosis, psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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antiinflammatory; cardiant; circulatory; antidiabetic; laxative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.6%; Score 1403.5; DB 5; Length 390; 69.1%; Pred. No. 1.7e-137; ive 40; Mismatches 78; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLCHRRFQKAFWKILCVTKQPAPSQ-TQSVSS 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mobilization, mitogenic effects, etc
                                                                                                                                                                                                                                                                                                        Claim 2; Page 16-17; 21pp; English.
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Matches 271; Conservative
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                                                                   WPI; 2002-673827/72.
                                                                                                   N-PSDB; ABW78739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 390 AA;
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The present sequence is that of a human histamine receptor of the H4
subtype, as predicted from a cDNA clone isolated from a bone marrow cDNA
library. The invention provides mammalian (human, mouse, rat and guinea
pig) histamine H4 receptor nucleic acid molecules (see AA170980-8) and
polypeptides (see AAM50564-67). The nucleic acids have been expressed in
recombinant host cells that produce active recombinant protein. The
paramacology of known histamine ligands is demonstrated. Mammalian
histamine H4 receptor may be used in gene therapy for the treatment of
diseases where it is beneficial to elevate mammalian histamine H4
ceceptor activity. Recombinant protein is useful for identifying
modulators of the human histamine H4 receptor. Such modulators may be
useful for diagnosing, treating or preventing asthma, allergy,
inflammation, cardiovascular and cerebrovascular disorders, non-insulin
dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,
disorders of the neuroendocrine system, stress and spasticity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 SFLEFVIPVILVAYFNMNIYWSLWKRDHLSRCQSHPGLTAVSSNICGHSFRGRLSSRRSL
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                                                                                                                                                                                                                                                                                                                                                                    New mammalian histamine H4 receptor proteins and polynucleotides the proteins, useful in gene therapy for treating diseases where beneficial to elevate mammalian histamine H4 receptor activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68.6%; Score 1403.5; DB 5; Length 390; 69.1%; Pred. No. 1.7e-137; Live 40; Mismatches 78; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 13; Fig 2; 92pp; English
                                                                                                                                                                                                                           (ORTH ) ORTHO-MCNEIL PHARM INC
                                                                                                                                        22-FEB-2001; 2001WO-US005914.
                                                                                                                                                                                  31-MAY-2000; 2000US-0208260P
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                                                          WO200192485-A1.
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prevent a disorder associated with the function of H4 in peripheral blood leukocytes. The present sequence represents the human histamine H4 receptor protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of human G-protein coupled receptor TGR62 protein.
                                                                                                                                                                                                                              1 MSESNGTDVLPLTAQVPLAFLMSLLAFAITIGNAVVILAFVADRNLRHRSNYFFLNLAIS
                                                                                                                                                                                                                                                       1 MPDTNSTINLSLSTRVTLAFFMSLVAFAIMLGNALVILAFVVDKNLRHRSSYFFLNLAIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, G-protein coupled; receptor; GPCR; TGR62; kidney disease; signal transduction modulator; cerebral cavernous malformation; hyperlipidemia; obesity; dyslexia; cardiac myxoma; renal failure; nephritis; hypertension; liver disease; cirrhosis; blood disorder; spleen-associated disorder; immune disorder.
                                                                                                                                      68.6%; Score 1403.5; DB 5; Length 390; 69.1%; Pred. No. 1.7e-137; ive 40; Mismatches 78; Indels 3;
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Best Local Similarity 69.11
Matches 271; Conservative
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N-PSDB; ABK12959.
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                                                                                            Sequence 390 AA;
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                                                                                                                                                                                                                                                                     Histamine receptor; H4; antirheumatic; antiarthritic; immunosuppressive; antiasthmatic; antiallergic; neuroprotective; antidiabetic; human; cerebroprotective; cAMP modulator; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New histamine receptor, termed H4 useful for detecting H4 (ant)agonists for treating transplanted organ rejection, asthma, allergy, multiple sclerosis and rheumatoid arthritis.
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172. .196
                                                                                                                                                                                                                         Human histamine H4 receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                       AAG66023 standard, protein, 390 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; Fig 1; 66pp; English.
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23-AUG-2000; 2000US-0227567P.
13-NOV-2000; 2000US-0247855P.
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The present invention relates to a new G-protein coupled receptor (GPCR) polypeptide comprising greater than 70% amino acid sequence identity to the amino acid sequence of human GPCRS TGR62, TGR21, TGR3130.2, human TGR213 or TGR92, 80% amino acid sequence identity to mouse TGR18 or 90% amino acid sequence identity to mouse TGR18 or 64fined in the specification. The GPCR covalently linked to a solid phase is useful for identifying a compound that modulates signal transduction. The identified compounds are useful for treating kidney disease, cerebral cavernous malformations, hyperlipidemia, obesity, dyslexia and cardiac myxoma. The molecules of the invention are useful for diagnosing disorders or conditions such as venal failure, nephritis, nephrotic syndrome, asymptomatic urinary abnormalities, renal tubule defects, hypertension and nephrolithiasis, liver-related disease or condition e.g. cirrhosis, infiltrations, lesions, functional disorders and jaundice and spleenassociated disease and others. Modulation of the polypeptide of the invention is useful to treat or prevent any of the above conditions or diseases. The present amino acid sequence represents the human GPCR TGR5 protein of the invention. This sequence is one of seven novel G protein coupled receptors of the invention (AAU74904-AAU74911)
treating kidney disease,
modulators of signal transduction for treating kidne:
hyperlipidemia, obesity, dyslexia and cardiac myxoma
                                                                           Claim 26; Page 61; 78pp; English.
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Sequence 390 AA;

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Best Local Similarity 69.19 121 239 361 61 61 301 299 g 엄 요 g 용 ઠે ઠ ઠે ò 요 ઠે ò

PLCHRRFQKAFWKILCVTKQPAPSQ-TQSVSS 391 PLCHKRFOKAFLKIFCIKKOPLPSOHSRSVSS 390 ABG71960 standard; protein; 390 AA 359 RESULT 15 ABG71960

(first entry) 28-JAN-2003 ABG71960; 2X2X5X3XX

Human; receptor; G-protein coupled receptor; AXOR35; lymphocyte; Human G-protein coupled receptor AXOR35.

The invention relates to an isolated G-protein coupled receptor

polypeptide, AXOR35, (and its homologues and variants) and its encoding

polypucleotide (and its homologues, variants, complements and RNA

equivalents). Also included are an anti-AXOR35 antibody, an AXOR35

cypression vector, producing a recombinant host cell by introducing the

cypression vector, producing a recombinant host cell by introducing the

cypression vector and antibiting are promoting the function of

the host cell expressing AXOR35, identifying/screening for agonists or

antagonists of AXOR35 and inhibiting or promoting the function of

lymphocytes, macrophages, eosinophils, or neutrophils in diseased tissue,

by administering to the patient AXOR35 agonists or antagonists. The

agonist or antagonist identified is useful for treating a disease such as

macrophages, eosinophils, or neutrophils in diseased tissue such as an

cathmatic lung. AXOR35 or polymucleotide is useful in diagnostic assays,

for identifying compounds that are agonists or antagonists of AXOR35, as

vaccines, or for treating infections (bacterial, fungal, protozoan or

viral infections), transplant rejection, qastrointestinal disorders (such

as gastric ulcer), inflammatory bowel diseases (such as atopic

corritable bowel syndrome, voniting, inflammation (such as atopic

dermatitis), allergy, autoimmune (such as urinary retention),

psoriasis), urological diseases (such as urinary retention),

cardiovascular diseases (such as urinary retention),

cardiovascular diseases (such as encompanied or for the form of a protocopy or

disease), cough, renal diseases (such as renal ischemmia),

cough, renal diseases (such as renal ischemmia),

cough, renal diseases (such as renal ischemmia),

cough, renal diseases (such as renal ischemmia),

cough, renal diseases (such as renal ischemmia),

cough, renal diseases (such as renal ischemmia),

cough, renal diseases (such as renal ischemmia),

cough, renal diseases (such as and openions),

cough, renal diseases (such as and openion gastrointestinal disorder; gastric ulcer; inflammatory bowel disease; croin s disease; irritable bowel syndrome; vomiting; inflammation; attopic dermatitis; allergy; autoimmune disorder; rheumatoid arthritis; psoriasis; urological disease; urinary retention; cardiovascular disease; myocardial infarction; hypotension; hypertension; pulmonary disorder; chronic obstructive pulmonary disease; cough; renal disease; renal ischaemia; arteriosclerosis; atherosclerosis; psychosis; neurological disorder; migraine; anorexia; anxiety; schizophrenia; dyskinesia; Parkinson's disease; cancer; obesity; stroke; septic shock; Novel isolated G-protein coupled receptor polypeptide, AXOR35, useful for treating infections, gastrointestinal disorders, autoimmune disorders, urological diseases, cardiovascular diseases and cancer. eosinophil; neutrophil; infection; transplant rejection; × :: Graybill TL, graft versus host disease; osteoporosis. Fitzgerald L, Aubart KM, Bergsma DJ, Fitzgerald Michalovich D, Morrow DM, Zhu Y; (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC. Claim 1; Page 22; 24pp; English. 03-FEB-2000; 2000US-00497790. 20-OCT-2000; 2000US-00693761. 20-JUL-2001; 2001US-00910411 2003-074982/07. N-PSDB; ABS57063 US2002137054-A1 Homo sapiens. 02-NOV-1999; 26-SEP-2002

Sequence 390 AA;

Score 1403.5; DB 6; Length 390; Pred. No. 1.7e-137; 68.6**%**; 69.1**%**; Best Local Similarity Query Match

(such as migraine, anorexia, anxiety, schizophrenia), dyškinesias (such as Parkinson's disease), cancer, obesity, stroke, septic shock, graft versus host disease and osteoporosis. The present sequence represents

as Parkinson's disease)

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241 PGLKEPAASLH9ESPRGKSSLLVSLRTHMSGSIIAFKVGSFCRSESPVLHQREHVELLRG 300 139 SASTEVPASFHSERQRRKSSLMFSSRTKMNSNTIASKMGSFSGSDSVALHQREHVELLRA 298
                                                                                                                                                                           301 RKLARSLAVLLSAFAICWAPYCLFTIVLSTYRRGERPKSIWYSIAFWLOWFNSLINPFLY 360
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               1 MSESNGTDVLPLTAQVPLAFLMSLLAFAITIGNAVVILAFVADRNLRHRSNYFFLNLAIS 60
                        3; Gaps
78; Indels
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Matches 271; Conservative
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Search completed: August 3, 2005, 01:44:47 Job time : 168 secs

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Sequence 14, Appl
Sequence 2, Appli
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Copyright (c) 1993 - 2005
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Maximum Match 100%
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seq length: 200000000
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## ALIGNMENTS

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US-10-626-445-9

10s-10-626-445-9

1 Sequence 9, Application US/10626445

1 Sublication No. US20040248252A1

2 Sublication No. US20040248252A1

3 GENERAL INFORMATION:

APPLICANT: Lovenberg, Timothy

TITLE OF INVENTION: UNMABE: US/10/626,445

CURRENT APPLICATION NUMBER: US/10/626,445

CURRENT FILING DATE: 2003-07-23

PRIOR PELLING DATE: 2001-02-22

PRIOR PELLING DATE: 2000-05-31

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin version 3.2

SEQ ID NO 9-
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100.0%; Score 2045; DB 16; Length 391;
Best Local Similarity 100.0%; Pred. No. 1.1e-183;
Matches 391; Conservative 0; Mismatches 0; Indels 0;
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ORGANISM: Rattus rattus
US-10-626-445-9
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Sequence 8, Application US/10626445
Publication No. US20040248252A1
GENERAL INFORMATION:
APPLICANT: Liu, Changlu
TITLE OF INVENTION: DNAB Encoding Mammalian Histamine Receptor Of The H4 Subtype FILE REPERENCE: PRD-0032
FILE REPERENCE: PRD-0032
CURRENT APPLICATION NUMBER: US/10/626,445
CURRENT FILING DATE: 2003-07-23
PRIOR APPLICATION NUMBER: 09/790,849
                                                                                                                                                                                                               APPLICANT: Lovenberg, Timothy
APPLICANT: Lovenberg, Timothy
APPLICANT: Lovenberg, Timothy
APPLICANT: Liu, Changlu
IIILE OF INVENTION: DNAS Encoding Mammalian Histamine Receptor Of The H4 Subtype
FILE REFERENCE: PRD-0034
CURRENT APPLICATION NUMBER: US/10/626,398
CURRENT FILING DATE: 2003-07-23
PRIOR PPLICATION NUMBER: 09/790,849
PRIOR FILING DATE: 2001-02-22
PRIOR FILING DATE: 2001-02-31
PRIOR FILING DATE: 2000-05-31
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 391
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Best Local Similarity 100.0%; Pred. No. 1.1e-183;
Matches 391; Conservative 0; Mismatches 0; Indels 0;
PLCHRRFQKAFWKILCVTKQPAPSQTQSVSS 391
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                                                                                                                                                 ; Sequence 9, Application US/10626398; Publication No. US20050074841A1; GENERAL INFORMATION:
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US-10-626-398-9
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APPLICANT: Lovenberg, Timothy
APPLICANT: Lovenberg, Timothy
TITLE OF INVENTION: DNA9 Encoding Mammalian Histamine Receptor Of The TILE REFERENCE: PRD-0033
CURRENT APPLICATION NUMBER: US/10/626,126
CURRENT PILING DATE: 2003-07-23
PRIOR PILING DATE: 2001-02-22
PRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.2
SEQ ID NO 9: 27
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100.0%; Pred. No. 1.1e-183;
tive 0; Mismatches 0;
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// Publication No. US20050074770A1
// GENERAL INFORMATION:
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Matches 391; Conservative
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) ORGANISM: Rattus rattus
US-10-626-126-9
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US-10-626-126-9
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APPLICANT: Lovenberg, Timothy
APPLICANT: Liu, Changlu
TITLE De INVENTION: DNAS Encoding Mammalian Histamine Receptor Of The H4 Subtype
FILE REFERENCE: PRD-0034
CURRENT APPLICATION NUMBER: US/10/626,398
CURRENT FILING DATE: 2003-07-23
PRIOR FILING DATE: 2001-02-22
PRIOR FILING DATE: 2001-02-22
PRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIAN OFFER SEGO.05-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIAN OFFER SEGO.05-31
LENGTH: 391
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Best Local Similarity 84.7%; Pred. No. 1.6e-154;
Matches 331; Conservative 17; Mismatches 43;
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US-10-626-398-8
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APPLICANT: Lovenberg, Timothy
APPLICANT: Liu, Changlu
ITILE OF INVENTION: DNAB Encoding Mammalian Histamine Receptor Of The H4 Subtype
FILE REFERENCE: PRD-0033
CURRENT APPLICATION NUMBER: US/10/626,126
CURRENT PILING DATE: 2003-07-23
PRIOR PPLICATION NUMBER: 09/790,849
PRIOR FILING DATE: 2001-02-22
PRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.2
SEQ ID NO 8
LENGTH: 391
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84.7%; Pred. No. 1.6e-154;
iive 17; Mismatches 43;
                                                                                                                                                                                                               Query Match 84.8%; Score 1735; DB 16; Best Local Similarity 84.7%; Pred. No. 1.6e-154; Matches 331; Conservative 17; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLCHRRFQKAFWKILCVTKOPAPSOTOSVSS 391
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PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: 60/208,260
PRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN Version 3.2
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 8, Application US/10626126; Publication No. US20050074770A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 84.7%
Matches 331; Conservative
                                                                                                                                     ; TYPE: PRT
; ORGANISM: Mus musculus
US-10-626-445-8
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US-10-626-126-8
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US-10-626-126-8
                                                                                                                 LENGTH: 391
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US-09-875-076-14
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RKLARSLAVLLSAFAICWAPYCLFTIVLSTYRRGERPKSIWYSIAFWLQWFNSLINPFLY 360
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69.1%; Pred. No. 2.6e-123;
iive 40; Mismatches 78;
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                                                                     361 PLCHRRFQKAFWKILCVTKQPAPSQTQSVSS 391
                                                                                          PLCHRRFQKAFWKILCVTKWPALSQNQSVSS 391
                                                                                                                                                                                         Sequence 2, Application US/09812216
Publication No. US20020098539A1
GENERAL INPORMATTON:
APPLICANT: Behan, Jiang Xu
APPLICANT: Hedrick, Joseph A.
APPLICANT: Hedrick, Joseph A.
APPLICANT: Monsma, Frederick J. Jr.
APPLICANT: Monsma, Frederick J. Jr.
APPLICANT: Wannsma, Frederick J. Jr.
APPLICANT: Wang, Suke
APPLICANT: Umland, Shelby P.
APPLICANT: Umland, Shelby P.
APPLICANT: Umland, Shelby P.
APPLICANT: Umland, Shelby P.
APPLICANT: Wang, Suke
J. TILE REFERENCE: CN01069
CURRENT APPLICATION NUMBER: 09/414,010
PRIOR APPLICATION NUMBER: 09/414,010
PRIOR FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 2
SEQ ID NO 2
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Matches 271, Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
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121 SYRTQHTGVLKIVTLMVAVWVLAFLVNGPMILVSESWKDEGS--ECEPGFFSEWYILAIT 178
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| Sequence 14, Application US/09875076
| Publication No. US20030017528A1
| GENERAL OF CHONATION:
| APPLICANT: Chen, Ruoping T. APPLICANT: Liaw, Chen W. APPLICANT: Liaw, Chen W. APPLICANT: Liaw, Chen W. APPLICANT: Lia, I.Lin, I.Lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9; Length 390;
APPLICANT: Bergsma, Derk
APPLICANT: Fitzgerald, Laura
APPLICANT: Li, Xiatong
APPLICANT: Li, Xiatong
APPLICANT: Mi, Xiatong
APPLICANT: Mi, Xiatong
TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
FILE REPERBRUE: 2001-07-20
CURRENT FILING DATE: 2001-07-20
FRICR APPLICATION NUMBER: 09/693,761
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-02-03
PRIOR PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 2000-02-03
PRIOR PRIOR FILING DATE: 2000-02-03
PRIOR PRIOR PRIOR DATE: 2000-02-03
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US-09-910-411-2
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358

Sequence 2, Application US/099104111 Patent No. US20020137054A1

US-09-910-411-2

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299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWFNSFVNPLLY 358
                                    APPLICATION NUMBER: 60/156,634
FILING DATE: 1999-09-29
APPLICATION NUMBER: 60/156,653
                                                                                                                                            Sequence 14, Application US/09876252
Publication No. US20030018182A1
GENERAL INFORMATION:
                                                                                                                                                                                                                Karin
                                                                                                                                                                                              APPLICANT: Behan, Dominic P. APPLICANT: Lehmann-Bruinsma, APPLICANT: Chalmers, Derek T.
                                                                                                                                                                                                                                          Lowitz, Kevin P.
Lin, I-Lin
Dang, Huong T.
Chen, Ruoping
Liaw, Chen W.
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APPLICANT:
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PRIOR PAPLICATION NUMBER: 60/121,951
PRIOR PAPLICATION NUMBER: 60/123,946
PRIOR PILING DATE: 1999-03-12
PRIOR PILING DATE: 1999-03-12
PRIOR PILING DATE: 1999-03-12
PRIOR PILING DATE: 1999-03-12
PRIOR PILING DATE: 1999-05-28
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PRIOR PILING DATE: 1999-05-29
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PRIOR PILING DATE: 1999-05-29
PRIOR PELING DATE: 1999-00-19
PRIOR PELING DATE: 1999-10-01
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69.1%;
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Best Local Similarity 69.15
Matches 271; Conservative
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ORGANISM: Homo sapiens
US-09-875-076-14
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LENGTH: 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 RYRAQHTGILKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTEECEPGFVTEWYILAIT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 AFLEFLLPVSLVVYFSVQIYWSLWKRGSLSRCPSHAGFIATSSRGTGHSRRTGLACRTSL 240
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; Publication No. US20030032784A1
; GENERAL INFORMATION:
; APPLICANT: Lind, Peter
; APPLICANT: Lind, Peter
; APPLICANT: Wood: Linda S.
; TITLE OF INVENTION:
; APPLICANT: Wood: Linda S.
; TITLE OF INVENTION: No. US20030032784A1e1 G Protein-Coupled Receptors
; FILE REFERENCE: 00231regUS
; CURRENT APPLICATION NUMBER: US/09/652,165
; CURRENT FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: USSN 60/203,108
; PRIOR PILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; MADER OF SEQ ID NOS: 3
; SEQ ID NO 2
; SEQ ID NO 2
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; Pred. No. 2.6e-123;
40; Mismatches 78; Indels 3;
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PRIOR PILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/157,280
PRIOR PILING DATE: 1999-10-01
PRIOR PILING DATE: 1999-10-01
PRIOR PILING DATE: 1999-10-01
PRIOR PILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,281
PRIOR APPLICATION NUMBER: 60/157,282
PRIOR APPLICATION NUMBER: 60/157,282
PRIOR PILING DATE: 1999-10-01
PRIOR PILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 146
NUMBER OF SEQ ID NOS: 146
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Best Local Similarity 69.1%;
Matches 271; Conservative 4
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US-09-876-252-14
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239 SASTEVPASFHSERQRRKGSLMFSSRTKMNSNTIASKONGSFSQSDSVALHQREHVELLRA 298
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                                                            78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Lin, Daniel Chi-Hong
APPLICANT: Lin, Daniel Chi-Hong
APPLICANT: Chen, Jin-Long
APPLICANT: Tularik Inc.
TITLE OF INVENTION: No. US20030083245Alel Receptors
FILE REPERENCE: 018781-006610US
CURRENT PILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/213,461
PRIOR APPLICATION NUMBER: US 60/213,461
PRIOR RELING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 26
SEQ ID NOS: 26
LENGTH: 390
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  68.6%; Score 1403.5; DB 1
69.1%; Pred. No. 2.6e-123;
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                                                            40; Mismatches
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Query Match
Best Local Similarity 69.1%
Matches 271; Conservative
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Query Match 68.6%;
Best Local Similarity 69.1%;
Matches 271; Conservative 4
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US-10-225-567A-629
                RESULT 14
JS-10-225-567A-629
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121 SYRIQHIGULKIVILMVAVWVLAFLVNGPMILVSESWKDEGS--ECEPGFPSEWYILAIT 178
                                                                       241 PGLKEPAASLHSESPRGKSSLLVSLRTHMSGSIIAFKVGSFCRSESPVLHQREHVELLRG 300
                                                                                                                             239 SASTEVPASFHSERQRRKSSLMFSSRTKWNSNTIASKMGSFSQSDSVALHQREHVELLRA 298
                                                                                                                                                                    301 RKLARSLAVLLSAFAICWAPYCLFTIVLSTYRRGERPKSIWYSIAFWLQWFNSLINPFLY 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78; Indels
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US-10-052-193-2

Sequence 2, Application US/10052193

Publication No. US20020132755A1

GENERAL INFORMATION:

APPLICANT: Pfizer, Inc.

TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS

FILE REPERENCE: PC10963A

CURRENT APPLICATION NUMBER: US/10/052,193

CURRENT FILING DATE: 2002-01-17

PRIOR FILING DATE: 2002-01-17

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2
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69.1%; Pred. No. 2.6e-123;
iive 40; Mismatches 78;
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Matches 271; Conservative
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ORGANISM: Homo sapiens
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Sequence 629, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Christine L.
TITLE OF INVENTION: ANTIGENE PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: 08/10/225,567A
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR PILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patentin version 3.1
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69.1%; Pred. No. 2.6e-123;
ive 40; Mismatches 78; Indels
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Publication No. US20030148450A1
GENERAL INFORMATION:
APPLICANT: Chen, Ruuping
APPLICANT: Liaw, Chen W.; APPLICANT: Liaw, Chen W.; APPLICANT: Liaw, Chen W.; APPLICANT: Liaw, Chen W.; APPLICANT: Liaw, Chen W.; APPLICANT: Liaw, Chen W.; APPLICANT: Liaw, Chen W.; APPLICANT: Liaw, Chen W.; APPLICANT: Liaw, Chen W.; APPLICANT: Liaw, Chen W.; APPLICANTON: Human Orphan G Protein Coupled Reciplement PILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: US/99/417,044
; PRIOR APPLICATION NUMBER: 60/109,213
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61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASVYNIVLISYDRYLSVSNAV 120
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PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR PLING DATE: 1999-02-26
PRIOR PLING DATE: 1999-02-26
PRIOR PLING DATE: 1999-02-26
PRIOR PLING DATE: 1999-03-12
PRIOR PLING DATE: 1999-03-12
PRIOR PLING DATE: 1999-03-12
PRIOR PLING DATE: 1999-05-28
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Best Local Similarity 69.1%; Pred. No. 2.6e-123;
Matches 271; Conservative 40; Mismatches 78; Indels 3;
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Job time : 159 secs
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; ORGANISM: Homo sapiens
US-10-272-983-14
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Sequence Novel pol Sequence

OM protein

Run on:

Sequence:

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AF307973 Homo sapi
AF2281556 Homo sapi
AF229449 Homo sapi
AI36745 Homo sapi
AX76577 Sequence
AX301229 Sequence
BD095598 Novel gua
AB045370 Homo sapi
AX44934 Homo sapi
AX44934 Homo sapi
AB097512 Novel gua
AB07512 Novel gua
AB075886 Cavia por
AC111672 Mus muscu
AC007922 Homo sapi
AC007922 Homo sapi
AC007922 Homo sapi
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AF267537 Cavia por
AR104702 Sequence
AR135733 Sequence
BD235873 Isolated
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AC090244 Homo sapi
AP002476 Homo sapi
AP001327 Homo sapi
AY231164 Macaca mu
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AR217155 Sequence
BD086286 G protein
AF321910 Homo sapi
AB019000 Homo sapi
E39824 Novel guano
ARS59688 Sequence
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Liu,C., Wilson,S., Kuei,C. and Lovenberg,T.W.
Direct Submission
Submitted (12-MAR-2001) Molecular Pharmacology, The R.W. Johnson
Pharmaceutical Research Institute, 3210 Merryfield Row, San Diego,
CA 92121, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus histamine H4 receptor mRNA, complete cds AF358860
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Liu,C., Wilson,S., Kuei,C. and Lovenberg,T.W.
Comparison of human, mouse, rat, and guinea pig histamine
receptor suggests substantial species variation
                         AK199119
AK109119
AK109119
AK100163
AK100163
AK100164
AK100164
AK100164
AK100164
AK10164
AK101
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/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
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AP00244
AP001327
AY231164
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HSA298292
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AC131672
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AR104202
AR135733
BD235873
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                                                                                                          AX301763
BD015847
AF307973
AF325356
AF329449
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BC069136
AX549343
AF312230
BD097512
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AC009668
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AB053300
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-MODEL=frame+ p2n.model -DEV=xlp
-Q=/Cqm2 1/USPFTO spool p/USIO16626126/runat 02082005 155436 2005/app query.fasta_1.583
-Q=/Cqm2 1/USPFTO spool p/USIO16626126/runat 02082005 155436 2005/app query.fasta_1.583
-DB=GenEmbl -QFMT=fastap -SUFFIX=rege -MINMATCH=0.1_-LOOPCI=0 -LOOPEXT=0
-UNITS=bits -START=1 -EMD=-1 -MATRIX=blooun62 -TRANS=human40.cdi -LIST=45
-UOTALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=20000000
-USR=USIO626126_@CGN 1 1.5600 @runat 02082005 155436_2005 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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AF358859 Mus muscu
AC118386 Rattus no
AY008280 Homo sapi
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                         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                    nucleic search, using frame_plus_p2n model
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Maximum Match 100%
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Database :

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Total number

Searched:

Minimum DB Maximum DB

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/protein_id="AAK97380.1"
/db_xref="G1:15420535"
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/tb_stref="G1:154205"
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/tb_stref="G1
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Liu,C., Whilson,S., Kuei,C. and Lovenberg,T.W.
Direct Submisson,S., Suei,C. and Lovenberg,T.W.
Submitted (12-MAR-2001) Molecular Pharmacology, The R.W. Johnson
Pharmaceutical Research Institute, 3210 Merryfield Row, San Diego,
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Liu, C., Wel, C. and Lovenberg, T.W. Comparison of human, mouse, rat, and guinea pig histamine H4 receptor suggests substantial species variation
                                                                                                                                                                                                                                                                                                                                                                                                                                  TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle
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                                                      CCTGGATTAAAGGAACCAGCGCGTCCCTTCATTCAGAAAGTCCACGAGGAAAGAGCAGT
                                                                                                                                                           CTCCTGGTGTCCTTAAGGACTCACATGAGCGGTAGTATCATCGCCTTCAAAGTGGGTTCC
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/product="histamine H4 receptor"
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/organism="Mus musculus"
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/strain="BALB/c"
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NLRHRSNYFFLMLAISDFFVGVISIPLYIPHTLFNWNFGSGICMFWLITDYLLCTASV
YSIVLISYDRYĞSVSNAVRYRAÇHTGILKIVAÇMYAMILAFLVNGPNILASDSWNS
TYTEGCEPGFVTEWYILATAFLEFLLPVSLVYFSVQIYWSIMKRGSLISRCPSHAĞF
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KVGSPCRSESPVLHQREHVELLRGRKLARSLAVLLSAFAICWAPYCLFTIVLSTYRG
BRPKSIWYSIAFWLQWFNSLINPFLYPLCHRRPQKAFWKILCVTKQPAPSQTQSVSS"
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Conservative:
Mismatches:
Indels:
Gaps:
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8 Worley, Kr. C.

Direct Submission

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Baylor Plaza, Houston, TX 77030, USA

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Direct Submission

Baylor Plaza, Houston, TX 77030, USA

Rat Genome Sequencing Consortium.

Direct Submission

Nov 15, 2002 this sequence version replaced gi:23812823.

The sequence on this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.twc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs are contage and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Yeleimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thingey, A., Trejos, Z., Usmani, K., Valas, R., Vara, V., Milasana, D., Waldon, L., Walker, B., Wang, G., Wang, S., Warren, J., Walrean, R., Wooden, H., Worley, F., Whilams, G., Williams, C., Wu, J., Zakub, S., Yen, J., Yoon, U., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Direct, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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183873 TACTGGAGCCTGTGGAAGCGTGGGAGTCTCAGTAGGTGCCCTAGCCACGCTGGATTCATC 183814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   320 ProTyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSer 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183813 GCTACCTCTTCCAGGGCACTGGACACTCACGCAGAACTGGGTTGGCTTGTAGGACAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183753 CTTCCTGGATTAAAGGAACCAGCCGCATCCCTTCATTCAGAAAGTCCACGAGGAAAGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 ValargTyrArgAlaGlnHisThrGlylleLeuLysIleValAlaGlnMetValAlaVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183933 ACAGCATTCTTGGAATTCCTGCTCCCTGTCTTGGTGGTCTATTTCAGTGTACAGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183693 AGTCTCCTGGTGTCCTTAAGGACTCACATGAGCGGTAGTATCATCGCCTTCAAAGTGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerPheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlyArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184113 GIGCGTTATAGAGCACAGCACACTGGCATCCTGAAAATTGTTGCTCAAATGGTGGCGCTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ThralaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIle
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272
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clone_end:Sp6"
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Best Local Similarity: 69.13% Mismatches: 77 Query Match: 68.73% Indels: 3 DB: 2	-10-626-126-9 (1-391) x AY008280 (1-1173)	Qy 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20 	Qy 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeuAlaPhe 40	Oy 41 ValalaAspargAsnLeuargHisArgSerAsnTyrPhePheLeuAsnLeualaIleSer 60	Qy 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80	Oy 81 AsnProGlySerGlyIleCysMetPheTrpLeulleThrAspTyrLeuLeuCysThrAla 100 :::	Oy 101 ServalTyrSerIleValLeuIleSerTyrAspArgTyrGInSerValSerAsnAlaVal 120	Oy 121 ArgTyrArgalaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTrp 140	Qy         141 IleLeuAlaPheLeuValAanGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160           ch         :::	161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaileThr   161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaileThr   161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaileThr	181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 20	201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPhelleAla	Db 595 röghöcöröröghadöcingarcarörörörörörörahöcöhörgarororöghorgar 654 Qy 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240	655 GTCTCTTCCAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT	Oy 241 ProGlyLubroAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260	Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280	Oy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300	Qy 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAla1leCysTrpAlaPro 320	AGGAGATTÁGCCAAGTCACTGGCCATTCTCTTÁGGGGTTTTTGCTGTTTGCTGGGGCTCCA 95	Oy 321 TyrCysLeuPheThr1leValLeuSerThrTyrArgArgGlyGluArgProLysSerlle 340
	<pre>Qy 340 IleTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeu 359                                      </pre>	Qy         360 TyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLys 379           Db         183393 TACCCTTGGGCAGACGTTTCAGAAGACTTTTCAGAAGACTTTTTGAGAAGATAATACTTGAGAAGACTTTTCAGAAGACTTTTTTTT	380 GlnProAlaProSerGlnThrGlnSerValSerSer 391	T 4 280	ATOUSZEU  ATOUSZEU  ATOUSZEU  ATOUSZEU  ACCESSION AY008280  VERSION AY008280.1 GI:15822540	ens (human) ens , Metazoa, Chordata,	REFERENCE 1 (bases 1 to 1173) AUTHORS Nguyen,T., Shapiro,D.A., George,S.R., Setola,V., Lee,D.K., Cheng,R., Rauser,L., Lee,S.P., Lynch,K.R., Roth,B.L. and		PUBMED 11179435 REFERENCE 2 (bases 1 to 1173) AUTHORS Nguyen,T., George,S.R., Lee,D.K., Cheng,R., Lynch,K.R. and O'nowd,R.P.	TITLE Discovery of H4, a Novel Histamine Receptor JOHRNAL Unpublished REPERBNCE 3 (bases 1 to 1173) AITHTORS Nature Coorte C D to D X Chang D Lunch K D and	O'Dowd, B.F. Direct Submission Submitted (26-SEP-2000) Pharmacology, University of Toron	FEATURES Location/Qualifiers  Source 1. 1173  /organism="Homo gapiens"	/mol_type="mRNA"	7	<pre>/gene="H4" /note="G protein-coupled receptor" /codon start=1 /</pre>	/product="nistamine receptor H4" /protein_id="AAL09297.1" /db_xref="G1:1582541" /translation="MADTNSTINLSLSTRVTLAPFMSLVAFAIMLGNALVILAFVVDK	NLRHRSSYFFNALAISOFPVGVISIPIYIPHTLEWDFCKEICVFWLTTDYLLCTASV YNIVLISYDRYLSYDRYLSYTDGHTGVLKIVTLMVAWVLAFLVNGPMILVSESWKDE GSECEPGFFSEWYILAITSFLEFUTPVILVAYFRNNIYWSLWKRDHLSRCOSHFCLTA VSSNICGHSFRGRLSSRRSLSASTEVPASFHSERQRRKSSLMFSSRTKWNSNTIASKM	GSFSQSDSVALHQREHVELLRARRLAKSTAILLGVFAVCWAPYSLFTIVLSFYSSATG PKSVWYRIAFWLQWFNSFVNPLLYPLCHKRFQKAFLKIFCIKKQPLPSQHSRSVSS" ORIGIN	nment Scores:	Pred. No.: 2.09e-107 Length: 1173 Score: 1405.50 Matches: 271 Percent Similarity: 79.59% Conservative: 41

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Histamine receptor receptor
Patent: US 6613533-A 1 02-SEP-2003;
Location/Qualifiers
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Sequence 1 from patent US 6613533.
AR391860
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/organism="unknown"
/mol_type="genomic DNA"
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1 (bases 1 to 1173)

Behan, J.X., Hedrick, J.A., Laz, T.M., Monsma, F.J., Umland, S.P. and Wang, S.
Polynucleotide encoding a histamine receptor
Patent: US 6204017-A 1 20 MAR-2001,
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/organism="unknown"
/mol_type="unassigned DNA"
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Best Local Similarity:
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Sequence 1 from Patent W00125432.
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Length:
Matches:
Conservative:
Mismatches:
Indels:
                               Gaps:
                                           (1-1173)
                                           (1-391) x AR391860
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Matches:
Conservative:
Mismatches:
Indels: DNA 1. .1173 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"

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121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTrp 140
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:

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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Location/Qualifiers
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                                          TCTTATAGAACTCAACATACTGGGGGTCTTGAAGATTGTTACTCTGATGGTGGCCGTTTGG 420
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G-protein coupled receptor-like polypeptide
Patent: EP 1096009-A 102-MAY-2001;
Pfizer Limited (GB) ; PFIZER INC. (US)
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Sequence 1 from Patent EP1096009.
AX139113.1 GI:14274791
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LOCUS
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Oy 81 AsnProGlySerGly1leCysMetPheTrpLeulleThrAspTyrLeuLeuCysThrAla 100 :::	Qy 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120 	Qy 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTrp 140	Qy       141 IleLeualaPheLeuValAsnGlyProMetIleLeualaSerAspSerTrpLysAsnSer 160         1:::	Qy 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180 :::	Qy 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200 :::	201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla	<pre>QY 211 IntserserargG1yIntG1yH18SerargArgIntG1yLeuAlacySArgIntSerLeu 240                                     </pre>	Qy 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260	Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPhelysValGlySer 280	Oy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300	Qy         301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro         320	321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 3	Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360 	Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380	Oy 381 ProAlaProSerGlnThrOlnSerValSerSer 391 	RESULT 10   BD015847   1173 bp   DNA   Linear PAT 27-AUG-2002   LOCUS   DBFINITION   Novel   Dolypeptide   ACCESSION   BD015847   G1:22556984   KEYWORDS   Homo sapiens   Homo sapiens   Homo sapiens   Homo sapiens   CRGANISM   Homo sapiens   Hom
Qy 281 PheCy8ArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300	Oy 301 ArglysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320	Oy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340	Oy 341 TrpTyrSerlleAlaPheTrpLeuGlnTrpPheAsnSerLeulleAsnProPheLeuTyr 360   11   1   1   1   1   1   1   1   1	Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380	Qy 381 ProAlaProSerGlnThrGlnSerValSerSer 391	RESULT 9 AX301763 LOCUS AX301763 1173 bp DNA linear PAT 30-NOV-2001 DEFINITION Sequence 1 from Patent W00185786.		ONGANISM Home sapiens (numan) ORGANISM Home sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.	ones, P.G., Blatcher, M., Wu, S. and uman histamine h 4? receptor atent: WO 0185786.A 1 15-NOV-2001;	FEATURES Incation/Qualifiers  Source //organism="Homo appiens" / / / / / / / / / / / / / / / / / / /	/db_xref="taxon:9606" ORIGIN	3.06e-107 1403.50 79.34%	Mismatches: Indels: Gaps:	MetSerGluSerAsnGlyTh	21 LeumetSerLeuLeualaPheAlaIleThrIleGlyAsnAlaValValIleLeualaPhe	4. Valaaspargasneurghishrgserasntyrphepheleuasnleualaileser 12. Grdordgacaaaaccricaagrachagriffffffffffffffffffffffffffffffffffff

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Homo sapiens (human)

ISM Homo sapiens

Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Rammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

CB 1 (bases 1 to 1173)

NS Jones, P. G., Wu, S. and Betty, M.

Cloning of a novel histamine receptor

VGE 2 (bases 1 to 1173)

DRS Jones, P. G., Wu, S. and Betty, M.

B Direct Submission

NAL Submitted (25-SEP-2000) Neuroscience, Wyeth Ayerst, CN8000,

Princeton, NJ 00543, USA

Location/Qualifiers

Source 1.1173
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GGTAGT-----GAATGTGAACCTGGATTTTTTTCGGAATGGTACATCCTTGCCATCACA
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    Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
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/organism='Homo sapiens (human)'
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
Bukaryota, Metazoa, Chordata, Craniata
Mammalia, Butheria, Primates, Catarrhi
1 (bases 1 to 1173)
Peter, B. and Olaylee, M.A.
Novel polypeptide
Patent: JP 2001211889-A 1 07-AUG-2001;
PPISER INC

    .1173
    /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

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1 (bases 1 to 1173)

Zhu, Y., Michalovich, D., Wu, H.-L., Tan, K.B., Dytko, G.M., Mannan, I.J., Boyce, R., Alston, J., Tierney, L.A., Li, X., Heritty, N.C., Vawter, L., Sarau, H.M., Ames, R.S., Davenport, C.M., Hieble, P., Wilson, S., Bergama, D.J. and Fitzgerald, L.R. Cloning, expression, and pharmacological characterization of a movel human histamine receptor

Mol. Pharmacol. 59 (3), 434-441 (2001)
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     221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu
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Zhu,Y., Michalovich,D. and Fitzgerald,L.R.
Direct Submission
Submitted (30-NOV-2000) GlaxoSmithKline, 709
1539, King of Prussia, PA 19406, USA:
Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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/map="18q11.2"
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VSSNICGHSFRGRLSSRRSLSASTEVPASFFSRQRRKSSLMFSSRTWMSNTIASKM
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RSSVGNSVALHQMFNSFVNPLLYPLCHKRPQKAFLKIFCIKKQPLPSQHSRSVSS"
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                                                                                                                        'note="G protein coupled receptor'
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Conservative:
Mismatches:
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GSECEPGFFSEWYILAITSFLEFVIPVILVAYFNMNIYWSLWKDBHLSRCQSHPGLTA
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1 (Dases 1 to 1173)
Morse, K.L., Behan, J., Laz, T.M., West, R.E. Jr., Greenfeder, S.A., Anthes, J.C., Umland, S., Wan, Y., Hipkin, R.W., Gonsiorek, W., Shin, N., and Monsma, F.L., Qiao, X., Wang, S., Hedrick, J.A., Greene, J., Bayne, M. and Monsma, F.J. Jr.
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Submitted (15-DEC-2000) Human Genomics Research, Schering-Plough
           TCTGCATCGACAGAAGTTCCTGCATCCTTTCATTCAGAGAGACAGAGGAGAAGAGTAGT 774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProbeuCysHisArgAheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln
                                                                                                                                                                                                         TTCTCCCAATCAGATTCTGTAGCTCTTCACCAAAGGGAACATGTTGAACTGCTTAGAGCC
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Monsma,F.J. Jr., Wang,S., Behan,J., Laz,T.M., Greene,J.
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    1173
/note="G-protein coupled receptor"

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Homo sapiens histamine receptor H4 mRNA,
AF329449
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1173 bp mRNA linear PRI 03-SEP-2002
Homo sapiens histamine receptor H4 (HRH4) mRNA, complete cds.
AY136745.1 GI:22658472
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                                                                                                                                  341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360
                                                                                                                                                                                        ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
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1 (bases 1 to 1173)
Puhl, H.L. III, Ikeda, S.R. and Aronstam, R.S.
Direct Submission
Submitted (26-JUL-2002) CDNA Resource Center, Guthrie Research Institute, One Guthrie Square, Sayre, PA 18840, USA
Location/Qualifiers
                          955 TATTCTCTGTTCACAATTGTCCTTTCATTTTATTCCTCAGCAACAGGTCCTAAATCAGTT
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                                                                                  TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle
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GSFSQSDSVALHQREHVELLRARRLAKSLAIILCVFAVCWAPYSLFTIVLSFYSSATG
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FKSVWYRIAFWLQWFNSFVNPLLXPLCHKRPQKAFLKIFCIKKQPLPSQHSRSVSS"
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Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (11-JAN-2001) O'Reilly M.A., Discovery Biology, Pfizer
Ltd, Ramsgate Road, Sandwich, Kent, CT13 9NJ, UNITED KINGDOM
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                          Identification of a histamine H4 receptor on human eosinophils Role in eosinophil chemotaxis Unpublished
2 (bases 1 to 1173)
O'Reilly, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGCCAGATACTAATAGCACAATCAATTTATCACTAAGCACTCGTGTTACTTTAGCATTT

1 ATGCCAGATACTAATAGCACAATTTATCACTAAGCACTCGTGTTACTTTAGCATTT
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receptor H4 (HRH4 gene).
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Conservative:
Mismatches:
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                     ProAlaProSerGln --- ThrGlnSerValSerSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="AML14.3D10"
                                                                                                                                Homo sapiens mRNA for histamine AJ298292
                                                                                                                                                                                                             gene
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Mammalia; Butheria; Primates;
                                                                                                                                                                                 AJ298292.1 GI:18152452
histamine receptor H4; HRH4
Homo sapiens (human)
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Aad01124 Human orp
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Ab280663 Human his
Ab278139 Nucleotid
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Ad982526 Human cDN
Ad98251663 Human cDN
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Aax70886 Human G-P
Aax0637 Human G-P
Aax06386 Human G-P
Aax0637 Human G-P
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                                    ABQ78739
AAI70980
AAI67750
ACA93262
ADG98759
ABS57063
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AAH47911
ABZ42573
ADO05719
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ADO29966
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AAI70982
  Command line parameters:
-MODEL=frame+_pzn.model_-DEV=xlp
-MODEL=frame+_pzn.model_-DEV=xlp
-MODEL=frame+_pzn.model_-DEV=xlp
-G=C=Gn2_1/USFTO_gpool_pUS10626126/runat_02082005_155435_1995/app_query.fasta_1.583
-DB=N_Geneseq_16Dec04_-QFMT=fastap_-SUFFTX=rng_-MINMATCH=0.1_-LOOPGI=0
-LOOPEXT=0_-UNITS=bits_-START=1_-END=-1_-MATRIX=blosum62_-TRANS=human40.cdi
-LIST=45_-DOCALIGN=200_-THR_SCORE=pct_-THR_MAX=100_-THR_MIN=0_-ALIGN=15
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-USRR=USI0656126_GCGN_1_1_708_Grunat_02082005_155435_1995_-NCPU=6_-ICPU=3
-NO_MMAP_-LARGEQUERY_-NEG_SCORES=0_-MAIT_-DEPBLOCK=100_-LONGLOG
-DEV_TIMEOUT=120_-WARN_TIMEOUT=30_-THREADS=1_-XGAPDEXT=0_-CAGAPEXT=0_5_-FGAPDOP=6
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Aad55126 Human H4
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           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                 nucleic search, using frame_plus_p2n model
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iant; circulatory; antidiabetic; laxative;
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                          New mammalian histamine H4 receptor proteins and polynucleotides enc
the proteins, useful in gene therapy for treating diseases where it
beneficial to elevate mammalian histamine H4 receptor activity.
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The present sequence is that of a cDNA clone encoding a murine histamine receptor of the H4 subtype. The cDNA was isolated from a mouse spleen cond ilbrary. It shows 72.8 homology to the human H4 receptor coding region. The invention provides mammalian (human, mouse, rat and guinea pig) histamine H4 receptor nucleic acid have been expressed in recombinant host cells that produce active recombinant protein. The pharmacology of known histamine ligands is demonstrated. Mammalian histamine H4 receptor may be used in gene therapy for the treatment of diseases where it is beneficial to elevate mammalian histamine H4 receptor activity. Recombinant protein is useful for identifying modulators of the mammalian histamine H4 receptor. Such modulators may be used in gene therapy for diseases may be used in gene therapy for intention activity. Recombinant protein is useful for identifying modulators of the mammalian histamine H4 receptor. Such modulators may be useful for diagnosing, treating or preventing asthma, allergy, inflammation, cardiovascular and cerebrovascular disorders, non-insulin dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia, clienticity
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the proteins, useful in gene therapy for treating diseases where it is
beneficial to elevate mammalian histamine H4 receptor activity.
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P-PSDB; AAM50565
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Sequence 1176 BP; 263 A; 281 C; 269 G; 363 T; 0 U; 0 Other;

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ò	61		GlyValileSer	IleProLeuTyrileP	AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80	
QQ	181	-	GGTTTGATTTCC	ATTCCTCTGTACATCC	GACTICCTCGTGGGTTTGATTTCCATTCCTCTGTACATCCCTCACGTGTTGTTTAACTGG 240	
8	81		GlyIleCysMet	AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCy	ASPIVILEULEUCYSThrAla 100	
QQ	241		GGAATCTGCATG	TTTGGCTCATTACTG	AATTITGGAAGTGGAATCTGCATGTTTTGGCTCATAACTGACTATCTTTTGTGCACCGCA 300	
È	101	ω –	TleValLeuIle	SerTyrAspArgTyrG	erValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120	
ΩP	301	-₽	RATIGICCICATI	AGCTACGATCGATACC	CTGTCTACAATATTGTCCTCATTAGCTACGATCGATACCAGTTTCAAATGCTGTG 360	
ò	121		GlnHisThrGly	IleLeuLysIleValA	ArgTyrArgAlaGlnHisThrGlylleLeuLysIleValAlaGlnMetValAlaValTrp 140	
qq	361	_	CAACACACTGGC	ATCATGAAGATTGTTG	TCTTATAGGGCTCAACACACACACTGAAGAATGTTGCTCAAATGGTGGTTTGG 420	
È	141		PreuValAsnGly	ProMetIleLeuAlaS	IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160	
g G	421		TTGGTAAATGGC	CCGATGATTCTGGCTT	ATACTGGCTTTCTTGGTAAATGGCCCGATGATTCTGGCTTCAGATTCTTGGAAGAACAGC 480	
ò	161		GluCysGluPro	GlyPheValThrGluT	ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrlleLeuAlaIleThr 180	
ą a	481		SGACTGTGAGCCT	GGCTTTGTTACAGAGT		

murine; gene; ss

WO20040400000-A2 Mus musculus.

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Transgenic mouse; neurological disorder; adrenal gland disorder;

Transgenic mouse; neurological disorder; adrenal gland disorder;

Transgenic mouse; neurological disorder; adrenal gland disorder;

Transgenic mouse; neurological disorder; adrenal disorder;

Transgenic disorder; blood disorder; immune disorder; bone disorder;

Transgenic disorder; metabolic disorder; nutritive disorder; cancer;

Transgenic disorder; liver disorder; prostate disorder; testis disorder;

Transgenic disorder; prostate disorder; spleen disorder;

Transgenic disorder; thyroid disorder; pancreas disorder; spleen disorder;

Try disorder; thyroid disorder; nutiparkinsonian; antimanic;

Try costatic; antinflammatory; vasotropic; antidarhotic; antidabetic;

Try dermatological; antidacterial; antianaemic; antidabetic;

Try dermatological; antidicer; antithyroid; antiallergic; antidabetic;

Try minnosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;
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                                                                                                                                                                                                                                    CCTGGATTGAAGGAATCAGCTGCATCTCGTCACTCAGAAAGTCCTCGAAGAAGAAGAGCAGC
                                                                                                                                                                                                                                                                                                        901 AGGAAGCTAGCCAGGTCACTGCCATCTTTTGCCGCTTTTGCCATTTGCTGGGCTCCA
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181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr
                               541 AIGCICITGGAATICCIGCITCTGTCAICTGIGGCITATITCAAIGTACAGATITAC
                                                                                        601 TGGAGCCTGTGGAAGCGTAGGGCTCTCAGTAGGTGCCCTAGCCATGCTGGATTCTCCACT
                                                                                                                                        ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu
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Li F; Zeng H;

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The invention relates to human and mouse g protein-coupled receptors (GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention; methods of treating, proteins and nucleic acids of the invention; methods of seases, at ransgenic compounds useful in the treatment of GPCR-related diseases, at ransgenic mouse comprising a GPCR gene of the invention; a mouse comprising a transgenic mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived from the trassgene or in an endogenous GPCR gene; cells derived from the trassgenic of the invention; a mouse comprising a mutation in a different GPCR gene of the invention; and kits comprising a mutation in a different GPCR gene of the invention; and kits comprising a mutation in a different GPCR gene of the invention. The comprising a GPCR nucleic acid. The GPCR polymother of the invention. The used in the disgloses variants of the GPCR polypeptides and vectors comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may be used in the disgloses, treatment or prevention of a wide variety of disseases including neurological disorders (e.g., Alzheimer's disease, (alseases including neurological disorders of the colon or intestine of syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or myocardial infarction); immune disorders (e.g., autoinmune disorders (e.g., antimune disorders (e.g., autoinmune disorders (e.g., antimune disorders (e.g., antimune disorders (e.g., autoinmune disorders (e.g., antimune disorders (e.g., antimune disorders (e.g., autoinmune disorders (e.g., antimune disorders (e.g., antimune disorders (e.g., antimune disorders (e.g., autoinmune disorders) (e.g., autoinmune disorders) (e.g., autoinmune disorders) 
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                                                                                                                                                                                                                                                     Gaitanaris GA, Bergmann JB, Gragerov A, Hohmann J,
Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 151; SEQ ID NO 1360; 542pp; English.
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                                                                       09-SEP-2003; 2003WO-US028226
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P-PSDB; ADO29497.
                     13-MAY-2004
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Seguence 1538 BP; 357 A; 362 C; 340 G; 479 T; 0 U; 0 Other;

1538 332 17 42 0 Length: Matches: Conservative: Mismatches: Indels: Gaps: 1.13e-150 1742.00 89.26% 84.91% 85.18% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Query Match: DB:

LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyA6nAlaValIleLeuAlaPhe 2

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MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe

US-10-626-126-9 (1-391) x ADO30257 (1-1538)

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AGGAAGCTAGCCAGGTCACTGGCCATCCTTCTGAGCGCTTTTGCCATTTGCTGGGCTCCA 1020 TACTGTCTGTTCACAATTGTCCTTTCAACTTACCCCAGAACGCACCCCCAAATCGGTG 1080 cerrirereredesecerrirecasaasecrrireresaasaraerrirereraaseaa 1200 240 960 TyrCysLeuPheThrlleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360 ProLeuCysHishrgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380 140 480 160 540 180 9 200 99 720 780 260 840 280 900 300 320 240 300 100 120 420 121 TTAATGTCTTCATTTGCCTTTGCTATAATGGTAGGCAATGCTGTGGTCATCTTAGCCTTT 180 9 8 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu TTCTGGCGATCGGAAAGTGCAGCGCTTCGCCAAAGGGAGTACGCAGAGGCTTCTCAGAGGC AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 121 ArgTyrArgAlaGlnHisThrGly1leLeuLysIleValAlaGlnMetValAlaValTrp IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer ATGCTCTTGGAATTCCTGCTTCCTGTCATCTCTGTGGCTTATTTCAATGTACAGATTTAC TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla Accretriceagracertraceacadadagacreagagaragaragagaraar LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer GACTICCTCGTGGGTTTGATTTCCATTCCTCTGTACATCCTCCTCGGGGTGTTTTAACTGG ATACTGGCTTTCTTGGTAAATGGCCCGATGATTCTGGCTTCAGATTCTTGGAAGAACAGC ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIJeLeuAlaIleThr 541 ACGAACACAAAAGGACTGTGAGCCTGGCTTTGTTACAGAGTGGTACATCCTCACCATTACA 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer cercearreaaggaarcagerecarcececacagaaagreeregaagaagageage Arccrosiorcernaagaacroardaacagcagrarcacrocerroaaagrosorroc PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 181 GTGGTGGACAGAAACCTTAGACATCGAAGTAATTATTTTTTTCTTAATTTGGCTATTTCT AspPhePheValGlyVallleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp aattttggaagtggaatctgcatgttttggctcattactgactatcttttgtgcaccgca SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 391 ProAlaProSerGlnThrGlnSerValSerSer 1021 1081 61 421 481 601 841 961 341 361 1141 381 41 241 81 301 101 141 161 201 221 721 241 781 261 281 901 301 321 661 g ò 셤 à a ò 셤 ઠે 셤 ઠે 셤 ઠે g ઠે 요 ઠે ద ઠે 임 ઠે 셤 8 셤 ò q ઠે 셤 ò 요 ઠે 셤 ઠે 셤 8 8

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                  AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp
                                                                                                                                                                         181 GACTTCTTTGTGGGTGTGATCTCCATTCCTTTGTACATCCCTCACACGCTGTTCGAATGG
                                                                                                                                                                                                          AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         il splice variants of human H4 histamine receptor, H4b and H4c, useful identifying agonists or antagonists of the receptor which are useful treating multiple sclerosis, asthma, allergy, psoriasis and stroke.
                                                                                                                                                                                  Human; H4; histamine receptor; inflammatory bowel disease; psoriasis; atopic dermatitis; stroke; myocardial infarction; migraine; allergy; chronic obstructive pulmonary disease; COPD; cerebroprotective; therapy; rheumatoid arthritis; multiple sclerosis; inflammation; neuroprotective; asthma; receptor; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to splice variants of human H4 histamine receptor H4b and H4c. The invention is useful for identifying an agonist, antagonist or inverse agonist of a mammalian histamine receptor. The agonist, antagonist or inverse agonist of H4b and H4c is useful for treating inflammation, asthma, allergy, atopic dermatitis, stroke, myocardial inflammation, migraine, chronic obstructive pulmonary disease (COPD), rheumatoid arthritis, multiple sclerosis, inflammatory bowel disease, or psoriasis. The present sequence is human H4 receptor DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP; 292 A; 245 C; 231 G; 402 T; 0 U; 0 Other
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/product= "Human H
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/partial
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13-NOV-2001; 2001US-0332697P
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                                                                                                                    (first entry)
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P-PSDB; AAE36417.
                                               AAD55126 standard;
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Pred. No.:
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DB:
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ProLeuCysHisArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln ccarrigricacaagcccrrrcaaagccrrrrcrrgaaarrarrrgraaaaaagccaa

361

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MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe

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ProAlaProSerGln---ThrGlnSerValSerSer 391

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    invention
  unknown (orphan GPCR receptors). More specifically the present inventior relates to non-endogenous, constitutively activated versions of a human GPCR. These non-endogenous human GPCRs can be useful for the direct identification of candidate compounds as receptors agonists, inverse agonists or partial agonists for use as pharmaceutical agents. AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in the exemplification of the present invention
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                             Human, G protein coupled receptor; GPCR; transmembrane receptor;
identification, agonist, screening; therapeutic; pharmaceutical; mutant;
                                                                                                                        G protein coupled receptor hRUP7 encoding cDNA SEQ ID NO:13
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Chalmers DT,
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9905-0151114P
9905-0155554P
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98US-0109213P.
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16-FEB-1999;
26-FEB-1999;
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                                                                                                                        Human
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The present sequence is a cDNA encoding hRUP7, an endogenous human orphan G protein-coupled receptor (GPCR). The full length hRUP7 cDNA was cloned by RT-PCR using human peripheral leucocyte cDNA as template. The orphan GPCR of the invention, like all GPCRs has seven transmembrane alpha helices with an extracellular N-terminus and an intracellular C-terminus. However, no endogenous ligands has yet been identified for the proteins of the invention. The orphan GPCRs may be used in the identification of their endogenous ligands, and to screen potential GPCR agonists and antagonists for use as pharmaceutical agents. The proteins may also be used in the study of GPCR-mediated signalling cascades, and to elucidate their precise role in normal and diseased human conditions. Nucleic acid encoding human orphan GPCRs may be used for tissue localisation expression analysis to provide information about their function in
                                                                                                                                                                                                                                                                  Novel human orphan G protein-coupled receptors and the encoding cDNAs for use in the identification of G protein-coupled receptor agonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 TTTATGTCCTTAGTAGCTTTTGCTATAATGCTAGGAAATGCTTTGGTCATTTTAGCTTTT 120
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ATGCCAGATACTAATAGCACAATCAATTTATCACTAAGCACTCGTGTTACTTTAGCATTT

ATGCCAGATACTAATAGCACAATCAATTTATCACTAAGCACTCGTGTTACTTTAGCATTTT
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99US-0157294P.
99US-00416760.
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01-OCT-1999;
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12-OCT-1999;
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CTCATGITTTCCTCAAGAACCAAGATGAATAGCAATACAATTGCTTCCAAAATGGGTTCC
                                                                                                     TTCTCCCAATCAGATTCTGTAGCTCTTCACCAAAGGGAACATGTTGAACTGCTTAGAGCC
                                                                                                                                                      ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro
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/note= "Human orphan G protein-coupled receptor"
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12-MAR-1999;
28-MAY-1999;
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28-MAY-1999;
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This cDNA of NCIMB 41073 encodes a human G-protein coupled receptor

(GPCR)-like polypeptide, designated PFI-013. The PFI-013 protein can be
expressed by standard recombinant methodology. Antibodies and modulators

of PFI-013 are useful in the manufacture of a medicament for treating

allergic disorder, including extrinsic asthma, immunological disorders,

and other pulmonary disease, including chronic obstructive pulmonary

disease (CPCPD), infectious, inflammatory disease, such as inflammatory

chasease (CPCPD), infectious, inflammatory disease, such as inflammatory

bowel disease and neoplastic and myeloproliferative diseases. They are

also useful for treating obesity, diabetes, metabolic, neurological

chiseases, psychotherapeutics, urogenital disease, reproduction and sexual

medicine, inflammation, cancer, tissue repair, dermatology, photoageing,

skin pjumentation, osteoprosels, cardiovascular, gastrointestinal

chiseases allergy and respiratory disease, sensory organ disorders, sleep

disorders and hair loss. The PFI-013 protein and nucleic acid are useful

chromial chasposis and treatment of the above conditions and also for

screening drug candidates for the treatment of diseases associated with

sugant transduction. The antibodies are also useful for enrichment of

consinous in the disposite of the above conditions and electing the

social and an enrichment of the conditions and also for

screening condidates for the treatment of diseases associated with

sugant transduction. The antibodies are also useful for enrichment of

conditions.
                                                                                                                                                                                                                                                                                                                                                                                       New G-protein coupled receptor-like polypeptide, polynucleotide for screening drug candidates for treating diseases associated with signal transduction e.g. allergic, inflammatory, pulmonary, neoplastic diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AspPhePheValGlyVallleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp
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1 ATGCCAGATACTAATAGCACAATCAATTTATCACTAAGCACTCGTGTTACTTTAGCATTT
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Mismatches:
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(PFIZ ) PFIZER INC.
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Best Local Similarity:
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GTGCTGGCCTTCTTAGTGAATGGGCCAATGATTCTAGTTTCAGAGTCTTGGAAGGATGAA 480
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histamine H3 receptor homologue; infection; viral; bacterial; fungal; protozoan; HIV-1; HIV-2; pain; cancer; diabetes; obesity; anorexia; butlimia; osteoporosis; asthma; allergy; urinary retention; acute heart failure; hypotension; hypertension; angina pectoris; myocardial infarction; stroke; ulcer; migraine; vomiting; psychotic disorder; neurological disorder; anxiety; schizophrenia; manic depression; bipolar disorder; anxiety; schizophrenia; severe mental retardation; dyskinesia; Parkinson's disease; dilles de la Tourette's syndrome; lymphocyte; macrophage; eosinophil; neutrophil; function modulation; autoimmune disorder; pulmonary disorder; gene therapy; vaccine; drug screening; signal transduction; transgenic animal; drug discovery;

'note= "G protein-coupled receptor"

/*tag= a /product= "Human AXOR35" Location/Qualifiers

sapiens.

Homo

AXOR35; human; G protein-coupled receptor; 7TM receptor;

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1015 TGGTATAGAATTGCATTTTGGCTTCAGTGGTTCAATTCCTTTGTCAATCCTTTTGTAT 1074
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The invention relates to the human G protein-coupled receptor AXOR35 (AAB73621), to cDNA encoding AXOR35 (AAB24006), and to AXOR35 fragments and variants. Like all G protein-coupled receptors, AXOR35 has transmembrane domains and is involved in signal transduction. AXOR35 has homology and structural similarity with G protein-coupled receptors such as the human histamine H3 receptor. The invention also relates to expression vectors and host cells comprising AXOR35 DNA, to recombinant expression of AXOR35, and to an AXOR35-specific antibody. AXOR35 proteins and nucleotides may be used to treat a wide variety of disorders including bacterial, fungal, protozoal and viral infections, particularly HIV-1 or HIV-2 infections; pain; cancers; benign prostatic hypertrophy; diabetes; obesity; anorexia; bulimia; osteoporosis; asthma; allergies; urinary retention; acute heart failure; hyperension; hypertension; angina urinary retention; acute heart failure; hyperension; hypertension; angina pectoris; myocardial infarction; stroke; ulcers; migraine; vomiting; psychotic and neurological disorders such as anxiety, schizophrenia, manic depression, depression, delirium, dementia, and severe mental retardation, depression, debression, debritum, dementia, and severe mental retardation, and dyskinesias, such as Parkinson's disease, Huntington's disease or Gilles de la Tourette's syndrome. AXOR35 proteins and nucleotides are useful as vaccines, and AXOR35 proteins, nucleotides and antibodies may be used in screening compounds for their ability to modulate AXOR35 activity or expression. Such AXOR35 modulators are particularly useful for treating asthma, and inhibiting or promoting the function of lymphocytes, macrophages, eosinophils or neutrophils in asthmatic lung. AXOR35 proteins, nucleotides and antibodies are also useful for diagnosing or determining susceptibility of an individual to a disease via the detection of abnormal levels of protein or mRNA, or via 

Human G protein-coupled receptor AXOR35 cDNA.

(first entry)

10-AUG-2001

AAH24007,

AAH24007
ID AAH2
XX
AC AAH2
XX
DT 10-7
XX
XX

AAH24007 standard; cDNA; 1173 BP

treating cancer, autoimmune, pulmonary, cardiovascular and neurological disorders and for identifying modulators useful for treating asthma. Novel G-protein coupled receptor polypeptide and polynucleotide for

Claim 2; Page 49-50; 54pp; English.

Ξ

Fitzgerald LR, Graybill TL,

SMIK ) SMITHKLINE BEECHAM CORP. SMIK ) SMITHKLINE BEECHAM PLC.

Aubart KM, Bergsma DJ, Fi Michalovich D, Morrow DM,

WPI; 2001-316464/33. P-PSDB; AAB73622.

26-OCT-2000; 2000WO-US029461. 02-NOV-1999; 99US-00431898. 03-FEB-2000; 2000US-00497790.

WO200133221-A1

10-MAY-2001

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the detection of mutations in the corresponding gene. AXOR35 proteins are also useful for inducing an immunological response in a mammal against the above diseases, and for antibody production. AXOR35 nucleotides are also useful as diagnostic reagents, in chromosome localisation and tissue expression studies, and for producing transgenic animals useful in drug discovery. AXOR35-specific antibodies are useful for purifying the AXOR35 protein or fragments thereof, and are also useful for treating conditions associated with the expression of the AXOR35 protein. The present
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È	201	TrpSerLe	TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla	lySerLeuSe	rArgCysPro	SerHisA	laglyPhel		220
qq	595	-	Gregaageere	ATCATCTCAG	raggiggea	AGCCATC	CTGGACTG	_	654
č	221	ThrSerSe	erSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu	lyHisSerArc	JArgThrGly	LeuAlaC	ysArgThr8		240
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                         ProLeuCysHisArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln
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                           This sequence represents the open reading frame for a human histamine receptor (HR) designated SP914. The sequence was isolated by searching databases with the sequence of known G-coupled protein receptor (GCPR). The gene is used for recombinant production of HR and for preparing antibodies (Ab). These Ab are used to purify HR by immunoaffinity clones that express the receptor, as antagonist to block binding of histamine for treating any histamine-associated disorder) and to generate anti-idiotypic antibodies. Agonists and antagonists of the HR protein can be used in the treatment of e.g. inflammation, asthma, allergy, atopic dermatitis, stroke, myocardial infarction, migraine, chronic obstructive pulmonary disease, rheumatoid arthritis, multiple sclerosis, inflammatory bowel disease and psoriasis
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Matches:
Conservative:
Mismatches:
Indels:
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          27-28; 19pp; English
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221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu
                                                                                          ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer
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MONSMA F J.
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                                 GGTAGT-----GAATGTGAACCTGGATTTTTTCGGAATGGTACATCCTTGCCATCACA
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antiinflammatory; cardiant; circulatory; antidiabetic; laxative;
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diagnosis; gene therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes a human histamine receptor. The polypeptide is useful for identifying an agonist or antagonist of a mammalian histamine receptor. It is useful as an antigen to elicit the production of antibodies. The histamine receptor polypeptide and polymucleotide are useful in the treatment and management of diseases such as inflammation, asthma, allergy, atopic dermatitis, stroke, myocardial infection, arthritis, multiple sciencists, pulmonary disease (COPD), rheumation, arthritis, multiple sciences, inflammatory bowel disease and psoriasis. They are also useful for modulating intracellular second messenger pathway activated through histamine receptors (cyclic-AMP, calcium, inositol phosphate and mitogen activated protein (MAP) kinase), changes in callular growth rate, secretion of hormones, receptor-stimulated Ca2+
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                                                                                                                                                                                                                                                                                                                            Example 1, Page 15-16; 21pp; English.
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                                                                            TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla
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                                                                                                        New mammalian histamine H4 receptor proteins and polynucleotides encoding the proteins, useful in gene therapy for treating diseases where it is beneficial to elevate mammalian histamine H4 receptor activity.
                                                                                                                                                                                                                                    histamine receptor of the H4 subtype. The cDNA was isolated from a bone marrow CDNA library. The invention provides mammalian (human, mouse, rat and guinea pig) histamine H4 receptor nucleic acid molecules (see AANT080-83) and polypeptides (see AAMS0564-67). The nucleic acids have been expressed in recombinant host calls that produce active recombinant protein. The pharmacology of known histamine ligands is demonstrated. Nammalian histamine H4 receptor may be used in gene therapy for the treatment of diseases where it is beneficial to elevate mammalian histamine H4 receptor activity. Recombinant protein is useful for identifying modulators of the human histamine H4 receptor Such modulators may be useful for diagnosing, treating or preventing asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 allergy, inflammation, cardiovascular and cerebrovascular disorders, non-
insulin dependent diabetes mellitus, hyperglycemia, constipation,
arrhythmia, disorders of the neuroendocrine system, stress and spasticity
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                                                                                                                                                                                                                          a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
                                                                                                                                                                                                                          present sequence is that of cDNA clone pH4R encoding
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The invention provides an isolated histamine receptor, H4, which binds ligands comprising imidazole attached to amine by an alkyl chain. The H4 receptor can be expressed by standard recombinant methodology. Cells expressing H4 receptor protein at a detectable level can suppress cyclic adenosine monophosphate (cAMP) formation when contacted with the H4 receptor agonist. The H4 receptor and antibodies are used for identifying H4 receptor adoulators. Modulation of histamine H4 receptors is useful for treating transplanted organ rejection, asthma, allergies and autoimmune pathologies such as multiple sclerosis, type I diabetes, rheumatoid arthritis, cognitive and memory defects. The H4 receptor protein and nucleic acids are useful targets to identify drugs that are effective in treating disorders associated with histamine-regulated processes. Identification and isolation of H4 receptor provides for development of screening of modecules that interact with H4 receptors. Genetic variants of H4 can be used to disquase an H4 associated of sease as described above. The H4 receptor polymucleotide is useful to treat or provent a disorder associated with the function of H4 in peripheral blood is and an analyses.
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histamine H4 receptor protein
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hARE-5; hRUP3; hRUP5; hRUP7; hGPCRZ7; hARE-1; hARE-2; hPPR1; hG2A;
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appearing as ABU92259-ABU92277 (encoded by CDNAs ACA93256-ACA93274) named
hARE-3, hARE-4, hARE-5, HRUP3, hRUP5, hRUP7, hGPCRZ7, hARE-1, hARE
-2, hPPR1, hC2A, hCTN3, hCHN4, hCHN6, hCHN9, hCHN10 and hRUF4.

Also included are a plasmid comprising a vector and one of the CDNAs
above and a host call comprising the plasmid. The GPCRS are useful for
the direct identification of candidate compounds as inverse agonists,
agonists or partial agonists. In vitro and in vivo systems incorporating
CPCRs is useful for elucidating and understanding the roles these
receptors play in the human condition, both normal and diseased, as well
as understanding the role of constitutive activation as it applies to
understanding the signalling cascade. The CDNAs are useful for making a
probe for dot-blot analysis against tissue mRNA and/or RT-CR
identification of the expression of the receptor in tissue samples. The
present sequence is a cDNA encoding a GPCR of the invention
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lin I;
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                                                                                                               98US - 0109213P .
99US - 0120416P .
99US - 01213946P .
99US - 0123946P .
99US - 0133946P .
99US - 013443P .
99US - 013443P .
99US - 013412P .
99US - 0137127P .
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99US - 015655F .
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DANG H T.
LIAW C W.
LIN I.
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US2003017528-A1
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                                                                           06-JUN-2001;
                                                                                                                                                                            12-MAR-1999;
12-MAR-1999;
28-MAY-1999;
28-MAY-1999;
28-MAY-1999;
28-MAY-1999;
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Pred. No.:
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PheCysArgSerGluSerProValleuHisGlnArgGluHisValGluLeuLeuArgGly 300
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1 ATGCCAGATACTAATAGCACAATCAATTTATCACTAAGCACTCGTGTTACTTTAGCATTT
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                                                                                               MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe
                                                                                                                                                                                                                                                           AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp
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    Conservative:
Mismatches:
Indels:
                                                                    (1-1173)
                                                                      x ADG98759
 79.34%
69.13%
68.63%
                                                                    US-10-626-126-9 (1-391)
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides novel human G protein-coupled receptor (GPCR) proteins and their encoding nucleic acids. The invention is useful for making a probe for dot-blot analysis and for XT-PCR identification of the expression of the receptor in tissue samples. The invention is also useful for identifying candidate compounds as inverse agonists, agonists to partial agonists and as research tools in determining the location of the receptors within the body. The present sequence is human orphan G protein-coupled receptor cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New cDNA encoding a human G protein coupled receptor, useful for making probe for dot-blot analysis against tissue-mRNA, and/or for RT-PCR identification of the expression of the receptor in tissue samples.
                                                                                                                                                    83
                                                                                                                                                   Human; G protein-coupled receptor; GPCR; research tool; gene;
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                                                                                                                                                                                                    Location/Qualifiers
1. .1173
/*tag= a
/product= "Human GPCR protein"
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Matches:
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                                          BP
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99US-012184EP.
99US-0123946P.
99US-0123946P.
99US-0136437P.
99US-0136437P.
99US-0136437P.
99US-0136437P.
99US-0136437P.
99US-014448P.
99US-0141448P.
99US-015655FP.
                                        ADG98759 standard; cDNA; 1173
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1403.50
                                                                                                                       Human orphan GPCR cDNA, RUP7
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P-PSDB; ADG98760.
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DANG H T.
LIAW C W.
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12-MAR-1999;
28-MAY-1999;
28-MAY-1999;
28-MAY-1999;
28-MAY-1999;
28-MAY-1999;
28-MAY-1999;
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16-FEB-1999;
26-FEB-1999;
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29-SEP-1999;
12-OCT-1999;
                                                                                                                                                                             Homo sapiens
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Pred. No.:
Score:
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28-SEP-1999;
                                                                                            11-MAR-2004
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(DANG/)
(LIAW/)
(LINI/)
                                                                   ADG98759
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              RESULT 14
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                                                              TATTCTCTGTTCACAATTGTCCTTTCATTTTATTCCTCAGCAACAGGTCCTAAATCAGTT 1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; se; gene; G-protein coupled receptor; AXOR35; lymphocyte; macrophage; eosinophil; neutrophil; infection; transplant rejection; gastrointestinal disorder; gastriculcer; inflammatory bowel disease; Crohn's disease; irritable bowel syndrome; vomiting; inflammation; atopic dermatitis; allergy; autoimmune disorder; rheumatoid arthritis; psoriasis; urological disease; urinary retention; cardiovascular disease; myocardial infarction; hypotension; hypertension; pulmonary disorder; chronic obstructive pulmonary disease; cough; renal disease; arteriosclerosis; atherosclerosis; psychosis; psychosis; dyskinesia; parkinson's disease; cancer; obesity; stroke; septic shock;
                                                                                                                        ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated G-protein coupled receptor polypeptide, AXOR35, useful for treating infections, gastrointestinal disorders, autoimmune disorders, urological diseases, cardiovascular diseases and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated G-protein coupled receptor polypoptide, AXOR35, (and its homologues and variants) and its encoding polymucleotide (and its homologues, variants, complements and RNA equivalents). Also included are an anti-AXOR35 antibody, an AXOR35
                                          TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cDNA encoding G-protein coupled receptor AXOR35,
                                                                                                                                                                                                                                      1135 CCTCTACCATCACACACAGTCGGTCAGTATCTTCT 1170
                                                                                                                                                                                                             ProAlaProSerGln---ThrGlnSerValSerSer 391
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03-FEB-2000; 2000US-00497790.
20-OCT-2000; 2000US-00693761.
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P-PSDB; ABG71960.
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cc expression vector, producing a recombinant host cell by introducing the vector into a cell such that the host cell produces AXOR35, a membrane of the host cell expressing AXOR35, identifying/screening for agonists or antagonists or antagonists or antagonists or by administering to the patient AXOR35 agonists or antagonists. The agonist or antagonist in diseased tissue, by administering to the patient AXOR35 agonists or antagonists. The agonist or for inhibiting or promoting the function of lymphocytes, as the acrophages, eosinophils, or neutrophils in diseased tissue such as an asthmatic lung. AXOR35 or polymuclectide is useful in diagnostic assays, for identifying compounds that are agonists or antagonists of AXOR35, as vaccines, or for treating infections (bacterial, fungal, protozoan or viral infections), transplant rejection, gastrointestinal disorders (such as gastric ulcer), inflammatory bowel diseases (such as rheumatoid arthritis, as gastric ulcer), inflammatory bowel diseases (such as rheumatoid arthritis, psoriasis), urological diseases (such as urinary retention), cardiovascular diseases (such as such as rheumatoid arthritis, disease), cough, renal diseases (such as renal ischemmia), cut alternation and diseases (such as recorders (such as majoraine, anoraxia, anxiety, setroke, septic shock, graft or arteriosclerosis, atherosclerosis, psychotic and neurological disease (such as majoraine), anoraxia, anxiety, setroke, septic shock, graft or arteriosclerosis, atherosclerosis, psychotic and neurological disease and osteoporosis. The present sequence is the cDNA
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TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPhelleAla 220
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-MODEL=frame+ p2n.model -DEV=xlp
-G=Cgn2 1/USPTO spool p/US10626126/runat_02082005_155437_2038/app_query.fasta_1.583
-G=Cgn2 1/USPTO spool p/US10626126/runat_02082005_155437_2038/app_query.fasta_1.583
-DS=Published Applications NA -QFPMT=fasta_ -SUPFIX=rnpb -MINNATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITG=bits -START=1 -RND=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR MAXE=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=PEDC -NORM=ext -HEAPGIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10626126 @CGN 1 1 723 @runat_02082005 155437_2038
-NCPU=6 -ICPU=3 -NO MMAP -LAGREQUERY NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DBY TINEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPPOR=10 -XGAPEXT=0.5
-FGAPOP=6 -FGĀPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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_6/ptodata/2/pubpna/US11_NEW_PUB.seq. _6/ptodata/2/pubpna/US60_NEW_PUB.seq. 6/ptodata/2/pubpna/US60_PUBCOMB.seq

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	ouenbess soluenbess so	stamine Receptor Of The H4 Subtype
ID	US-10-626-445-6 US-10-626-445-6 US-10-626-445-6 US-10-626-445-6 US-10-626-445-5 US-10-626-446-5 US-10-626-446-5 US-10-626-446-5 US-10-626-418-5 US-10-626-418-5 US-10-910-411-1 US-09-910-411-1 US-09-910-411-1 US-10-910-411-1 US-10-910-611-1	11 / / / / / / / / / / / / /
e	11173 119 119 119 119 119 119 119 119 119 11	Sequence 6, Application US/10626; Publication NO. US2004024825211; GENERAL INFORMATION: APPLICANT: Lovenberg, Timothy APPLICANT: Liu, Changlu TITLE OF INVENTION: DNAS Encodi; FILE REFERENCE: PRD-0032; CURRENT APPLICATION NUMBER: US/CURRENT FILING DATE: 2003-07-2; PRIOR FILING DATE: 2001-02-22; PRIOR FILING DATE: 2001-02-22; PRIOR FILING DATE: 2000-05-31; NUMBER OF SEQ ID NOS: 27
% Query Match		Applicat No. US20 No. US20 No. US20 Lovenber, Liu, Ch Liu, Ch SNCE: PRD LICATION LIGATION LIGATION G DATE: GCATION NO. SEQ ID NO.
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US-10-626-126-6
; Sequence 6, Application US/10626126
; Sequence 6, Application US/10626126
; Publication No. US20050074770A1
; GENERAL INPORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAS Encoding Mammalian Histamine Receptor Of The H4 Suring PREPRENCE: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626,126
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR FILING DATE: 2001-02-22
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 6
; LENGTH: 1176
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; SOFTWARE: Patentin v
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CURRENT APPLICATION NUMBER: US/10/626,398	Qy 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20	Oy 21 LeuMetSerLeuLeuAlaPheAlaileThrileGlyAbnAlaValileLeuAlaPhe 40	Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlalleSer 60	Oy 61 ASpPhePheValG1yVall1eSerIleProLeuTyrl1eProHisThrLeuPheAsnTrp 80	Oy 81 ASRProGlySerGlyIleCysMetPheTrpLeulleThrAspTyrLeuLeuCysThrAla 100	Oy 101 SerValTyrSerIleValLeuIleSerTyrAspargTyrGlnSerValSerAsnalaVal 120	Oy 121 ArgTyrArgAlaGlnHisThrGly11eLeuLyS11eValAlaGlnMetValAlaValArp 140	Qy         141 IleLeualaPheLeuValaanGlyProMetIleLeualaSerAspSerTrpLysAsnSer 160	Qy         161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrlleLeuAlaileThr 180	Qy 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200	Oy 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysBroSerHisAlaGlyPhelleAla 220	Oy 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlacysArgThrSerLeu 240	Qy 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
81   AsnProGlySerGlyIleCysMetPheTrDLeulIeThrAspTyrLeuLeuCysThrAla 100   101	Qy     201 TrpSerLeuTrpLyBArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla     220       IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240	Oy 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260	Oy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280	Oy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300	Qy       301 ArglysleualaArgSerleualaValLeuleuSeralaPhealaIleCysTrpalaPro       320         IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy       321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProiysSerIle 340         IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy       341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeulleAsnProPheLeuTyr       360         IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380	Oy 381 ProAlaProSerGlnThrGlnSerValSerSer 391 	RESULT 3 US-10-626-398-6 ; Sequence 6, Application US/10626398		; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype ; FILE REFERENCE: PRD-0034

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TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
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| Publication No. US200402482521
| GENERAL INFORMATION:
| APPLICANT: Lovenberg, Timothy
| APPLICANT: Liu, Changlu
| TITLE OF INVENTION: DNAS Encoding Mammalian His:
| FILE REFERENCE: PRD-003-07-23
| CURRENT APPLICATION NUMBER: US/10/626,445
| CURRENT FILING DATE: 2001-02-22
| PRIOR APPLICATION NUMBER: 60/208,260
| PRIOR FILING DATE: 2001-03-22
| PRIOR FILING DATE: 2001-05-31
| NUMBER OF SEQ ID NOS: 27
| SOFTWARE: Patentin version 3.2
| SEQ ID NO 556
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84.91%
85.18%
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-10-626-445-5
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APPLICANT: Lovenberg, Timothy
APPLICANT: Lovenberg, Timothy
APPLICANT: Liu, Changlu
TITLE OF INVENTION: DNAS Encoding Mammalian Histamine Receptor Of The H4 Subtype
FILE REFERENCE: PRO-034
CURRENT APPLICATION NUMBER: US/10/626,398
CURRENT FILING DATE: 2003-07-23
PRIOR PILING DATE: 2001-02-22
PRIOR FILING DATE: 2000-05-31
PRIOR FILING DATE: 2000-05-31
SOFTWARE: Patentin version 3.2
SEQ ID NOS: 27
SOFTWARE: Patentin version 3.2
SEQ ID NO 5
LUNGTH 1176
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                                       APPLICANT: Lovenberg, Timothy
APPLICANT: Liu, Changlu
TITLE OF INVENTION: DNAS Encoding Mammalian Histamine Receptor Of The H4 Subtype
FILE REFERENCE: PRD-0033
CURRENT APPLICATION NUMBER: US/10/626,126
CURRENT FILING DATE: 2003-07-23
PRIOR FILING DATE: 2001-02-22
PRIOR FILING DATE: 2001-02-22
PRIOR FILING DATE: 2000-05-31
PRIOR FILING DATE: 2000-05-31
SOFTWARE: Patentin version 3.2
SEQ ID NOS: 27
SOFTWARE: Patentin version 3.2
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Matches:
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Sequence 5, Application US/10626126
Publication No. US20050074770A1
GENERAL INFORMATION:
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1 ATGCCAGATACTAATAGCACAATCAATTTATCACTAAAGCACTCGTGTTACTTTTAGCATTT
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Matches:
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                               1141 CCAGCGCTGTCACAGAACCAGTCAGTATCTTCT
                ProAlaProSerGlnThrGlnSerValSerSer
                                                                                               Sequence 1, Application US/09812216
Patent No. US20020098539A1
GENERAL INFORMATION:
APPLICANT: Behan, Jiang Xu
APPLICANT: Hedrick, Joseph A.
APPLICANT: Mannsma, Frederick J. Jr.
APPLICANT: Morse, Kelley L.
APPLICANT: Worse, Kelley L.
APPLICANT: Wang, Suke
TITLE OF INVENTION: Histamine receptor
FILE REFRENCE: CON1069
FILE REPRENCE: CON1069
CURRENT APPLICATION NUMBER: US/09/812,216
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver: 2.1
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1403.50
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Query Match:
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; ORGANISM: HOMO
US-09-812-216-1
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  ORGANISM: Homo sapien
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                                 Alignment Scores
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Sequence 1. US20020137054A1

GENERAL INFORMATION:

APPLICANT: Fitzgerald, Laura

APPLICANT: Fitzgerald, Laura

APPLICANT: Michalovich, David

APPLICANT: Zhu, Xiatong

APPLICANT: Zhu, Yuan

ITILE OF INVENTION: AXOR35, A G-Frotein Coupled Receptor

FILE REFERENCE: GF70655-2C1

CURRENT APPLICATION NUMBER: US/09/910,411

CURRENT FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 09/497,790

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-02-03

PRIOR FILING DATE: 1999-11-02

NUMBER OF SEQ ID NOS: 2

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 1173
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Conservative:
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PRIOR APPLICATION NUMBER: 60/157,282
PRIOR FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 1173
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1403.50
79.34%
69.13%
                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
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Best Local Similarity:
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                      TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr
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  ArglysleuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro
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Us-09-875-076-13

Us-09-875-076-13

Sequence 13, Application US/09875076

PUBLICARTION NO. US20030017528A1

GENERAL INFORMATION:

APPLICANT: Chen, Runching

APPLICANT: Lin, Lin, Lin

TITLE OF INVENTION: Human Orphan G Protein Coup

FILE REPERENCE: ARENGOS

CURRENT FALING DATE: 1999-10-12

PRIOR PILING DATE: 1999-10-12

PRIOR PELING DATE: 1999-0-16

PRIOR PLING DATE: 1999-0-2-16

PRIOR PLING DATE: 1999-0-2-16

PRIOR PLING DATE: 1999-0-2-16

PRIOR PLING DATE: 1999-0-2-28

PRIOR PLING DATE: 1999-0-2-28

PRIOR PRIOR DATE: 1999-0-2-28

PRIOR PLING DATE: 1999-0-2-29

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Matches:
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: 60/136,436
PRIOR APPLICATION NUMBER: 60/136,436
PRIOR FILING DATE: 1999-05-28
PRIOR FILING DATE: 1999-05-28
PRIOR PELLING DATE: 1999-05-29
PRIOR PELLING DATE: 1999-05-29
PRIOR PELLING DATE: 1999-05-29
PRIOR PELLING DATE: 1999-09-29
PRIOR PELLING DATE: 1999-00-10
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PRIOR PELLING DATE: 1999-10-01
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ORGANISM: Homo sapiens
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Query Match:
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ORGANISM: Homo
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                                  IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer
                                            GIGCTGGCCTTCTTAGTGAATGGGCCAATGATTCTAGTTTCAGAGTCTTGGAAGGATGAA
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         TCTTATAGAACTCAACATACTGGGGTCTTGAAGATTGTTACTCTGATGGTGGCCGTTTGG
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| Publication No. US20020132755A1
| GENERAL INFORMATION:
| APPLICANT: PEffact, Inc.
| TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
| TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
| CURRENT APPLICATION WHOBER: US/10/052,193
| CURRENT APPLICATION NUMBER: 0101223.6
| PRIOR APPLICATION NUMBER: 0101223.6
| PRIOR APPLICATION NUMBER: 0101223.6
| PRIOR FILING DATE: 2001-01-17
| NUMBER OF SEQ ID NOS: 10
| SEQ ID NOS: 10
| SEQ ID NO 1
| LENGTH: 1173
| TYPE: DNA
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   4.25e-145
1403.50
79.34%
69.13%
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240 100 300 120 360 140 420

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321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
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                                                                                                                       41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer
                                                                                                                                           AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp
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                                                    21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe
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TyrCysLeuPheThr11eValLeuSerThrTyrArgArgGlyGluArgProLysSerI1e
                                                                                                                                      TrpTyrSerileAlaPheTrpLeuGlnTrpPheAsnSerLeulleAsnProPheLeuTyr
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    See File Wrapper or PALM

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APPLICANT: Chen, Ruoping
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, I-Lin
TITLE OF INVENTION: Human Orphan G Protein CC
FILE REFERENCE: ARENOSOG
CURRENT APPLICATION NUMBER: US/10/272,983
CURRENT FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 60/10/213
PRIOR PILING DATE: 1999-0-216
PRIOR PILING DATE: 1999-0-216
PRIOR PILING DATE: 1999-0-216
PRIOR FILING DATE: 1999-0-3-12
PRIOR PILING DATE: 1999-0-3-2
PRIOR PILING DATE: 1999-0-3-8
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Publication No. US20030148450A1
GENERAL INFORMATION:
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Best Local Similarity:
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APPLICANT: Dang, Huong T.
APPLICANT: Liaw, Chen W.
TILLE REPERENCE: ARENOSOS
CURRENT APPLICATION: Human Orphan G Protein Coupled Receptors
CURRENT APPLICATION NUMBER: US/10/393,807
CURRENT APPLICATION NUMBER: US/09/417,044
PRIOR APPLICATION NUMBER: 60/109,213
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR APPLICATION NUMBER: 60/121,851
PRIOR APPLICATION NUMBER: 60/121,851
PRIOR APPLICATION NUMBER: 60/123,946
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APPLICANT: Pfizer Inc.
APPLICANT: Pfizer Inc.
APPLICANT: O'Reilly, Mark A.
APPLICANT: O'Reilly, Mark A.
APPLICANT: Peter, Beate
FILE REFERENCE: PC10373B
CURRENT APPLICATION NUMBER: US/0/354,769
CURRENT APPLICATION NUMBER: US 09/698,801
PRIOR PILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1000-04-20
NUMBER OF SEQ ID NOS: 10
SEQ ID NOS: 10
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US-10-354-769-1
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Sequence 13, Application US/10417820A

Publication No. US20030229216A1

Sequence 13, Application US/10417820A

Publication No. US20030229216A1

SEMERAL INFORMATION:

APPLICANT: Liaw, Chen W.

APPLICANT: Lowitz, Kevin

APPLICANT: Lowitz, Kevin

APPLICANT: Lowitz, Kevin

APPLICANT: Behan, Dominic P.

ITILE OF INVENTION: Receptors

FILE REFERENCE: 7. US28. CON

CURRENT APPLICATION NUMBER: US/10/416, 760

PRIOR PILING DATE: 1999-10-12

PRIOR PILING DATE: 1999-10-22

PRIOR PILING DATE: 1999-10-27

PRIOR PILING DATE: 1999-02-16

PRIOR FILING DATE: 1999-02-16

PRIOR PILING DATE: 1999-03-12

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PRIOR FILING DATE: 1999-03-12
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PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,949
PRIOR FILING DATE: 1999-03-12
PRIOR PILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,437
PRIOR FILING DATE: 1999-05-28
PRIOR PILING DATE: 1999-05-28
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PROWARER OF SEC ID NOS: 74
SOFTWARE: PARENTH VET. 2.1
SECTION 13
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CORGANISM: Homo sapiens
US-10-393-807-13
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NUMBER OF SEQ ID NOS: 155
SOFTWARE: Patentin version
                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                               US-10-417-820A-13
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1074
                                                                                                                                                         ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
                                                                                                                    TrpTyrSerileAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360
                                                          954
                                                                             TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
                                     1015 TGGTATAGAATTGCCTTTTTCGTTTCAATTCCTTTGTCATTTGTAT
PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly
                                                                                                                                                                                                            CTCTACCATCACACACACAGTCGGTCAGTATCTTCT 1170
                                                                                                                                                                                                 ProAlaProSerGln---ThrGlnSerValSerSer 391
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Search completed: August 5, 2005, 17:38:06 Job time: 723 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 3, 2005, 01:38:32; Search time 41 Seconds (without alignments) 917.579 Million cell updates/sec

US-10-626-126-9 2045 1 MSESNGTDVLPLTAQVPLAF......WKILCVTKQPAPSQTQSVSS 391 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES æ

Description	histamine H4 recep	muscarinic acetylc		muscarinic acetylc	muscarinic acetylc	histamine H1 recep	muscarinic acetylc	muscarinic acetylc	histamine H1 recep	muscarinic acetylc	serotonin receptor		muscarinic acetylc	muscarinic acetylc	hypothetical prote	serotonin receptor	serotonin receptor	muscarinic recepto	muscarinic acetylc	histamine H1 recep	histamine H1 recep	serotonin receptor	alpha-1A-adrenergi	alpha-1A-adrenergi	alpha-1A adrenergi	serotonin receptor	alpha-1A adrenergi	muscarinic acetylc	alpha-1-adrenergic
ΙD	JC7566	S47572	S01114	A29476	S10128	A41632	JT0531	B29514	JC2495	JT0530	A42688	A24325	A55019	809508	T18863	S18637	JN0268	151837	A29514	JC1415	156507	S54153	JH0447	I39369	871323	S68422	A38731	A31897	A40491
DB	2	~	~	N	N	~	~	~	~	~	7	~	7	7	7	~	7	7	N	7	7	N	7	~	~	~	~	N	0
Length	390	590	590	589	290	491	531	589	487	532	386	460	639	460	501	386	390	460	460	486	488	386	501	572	477	389	260	460	515
Query Match	68.6	20.1	20.0	19.9	19.7		19.6	19.4	19.3	19.3	19.1	19.0	19.0	19.0	19.0	ω,	ω.	18.9	18.9	18.7	18.7	18.6	18.4	18.4	18.4	18.3		•	18.2
Score	1403.5	410.5	408.5	407.5	403.5	401.5	401	397.5	395.5	395	390.5	389.5	389	388.5	388	387.5	87.	385.5	385.5	383	82	380.5	377	377	375.5	374.5		373.5	372.5
Result No.	-	8	ń	4	S	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	58	53

serotonin receptor	alpha-1B adrenergi	serotonin receptor	alpha-1B-adrenergi	serotonin receptor	muscarinic acetylc	serotonin receptor	serotonin receptor	muscarinic acetylc	serotonin receptor	alpha-1C-adrenergi	alpha-1C-adrenergi	muscarinic acetylc	alpha-1C-adrenergi	muscarinic acetylc	G protein-coupled
S58126	A45121	A47385	JC1525	JC6178	S10126	A53279	S26048	833776	A47321	865656	JN0765	S10856	865657	A40972	B30341
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													17.5 499 2		
18.1		17.8			17.7				17.5	17.5		17.5		17.4	17.4

## ALIGNMENTS

	RESULT 1	
	107/566	UC/Sebs of A conserve units   human
	T.Speci.	
	C; Date:	
	C, Acces	C;Accession: JC7566
	R;Nakam	Y.; Ohta
	Biochem	
	A;Title A:Refer	Ajillie: Molecular Cioning and chalaccerization of a new numan nistamine receptor, hh4k. A.Reference number: JC7566: WUID: 20568725; PMID:1111834
	A; Conte	A; Contents: Leukocyte
	A; Acces	A,Accession: JC7566
	A; Molec	A; Molecule type: mm.
	A; Kesid	A;Kesilues: 1-350 (VANK> - Arkesilues: Inibor. Adding DDB1. ABA45370
	C; Comme	C; Comment: This receptor, belonging to the biogenic amine receptors of G protein-coupled
	C,Genetics:	
	A;Gene: hh4r C;Keywords: (	A;Gene: hh4r C;Keywords: G protein-coupled receptor; transmembrane protein
	Vierv	Ouery Match 68.6*: Score 1403.5: DB 2: Length 390:
	Best Local Matches 27	Similarity 69.1%; Pred. No. 7.4e-112; 1; Conservative 40; Mismatches 78; 1
	ò	1 MSESNGTDVLPLTAOVPLAFLMSLLAFAITIGNAVVILAFVADRNLRHRSNYFFLNLAIS 60
	<b>X</b>	
	ag	1 MPDTNSTINLSLSTRVTLAFFMSLVAFAIMLGNALVILAFVVDKNLRHRSSYFFLNLAIS 60
	δõ	61 DFFVGVISIPLYIPHTLFNWNPGSGICMFWLITDYLLCTASVYSIVLISYDRYQSVSNAV 120
	qq	61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASVXNIVLISYDRYLSVSNAV 120
	ò	121 RYRAQHTGILKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTEECEPGFVTEWYILAIT 180
_	•	
	q ₀	121 SYRTQHTGVLKIVTLMVAVWVLAFLVNGPMILVSESWKDEGSECEPGFFSEWYILAIT 178
	ò	181 AFLEFLIPVSLVVYFSVQIYMSLMKRGSLSRCPSHAGFIATSSRGTGHSRRTGLACRTSL 240
	qa	179 SFLEFVIEVILVAYFNMNIYWSLWKRDHLSRCQSHPGLTAVSSNICGHSFRGRLSSRRSL 238
	ò	241 PGLKEPAASLHSESPRGKSSLLVSLRTHMSGSIIAFKVGSPCRSESPVLHQREHVELLRG 300
	qa	239 SASTEVPASFHSERQRRKSSLMFSSRTKMASNTIASKWGSFSQSDSVALHQREHVELLRA 298
	ò	AVLLSAFAICWAPYCLFTIVLSTYRGERPK
	qa	299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWFNSFVNPLLY 358
	λō	361 PLCHRRPQKAFWKILCVTKQPAPSQ-TQSVSS 391
	qq	

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QTQSVSS 391
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muscarinic acetylcholine receptor m3 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 27-dan-1995 #sequence_revision 27-dan-1995 #text_change 09-Jul-2004
C;Datesesion: 847572
B;Cession: 847572
B;Chie, P.H.K.; Hodges, P.K.; Glickman, F.; Chang, K.J.
Biochim. Biophys. Acta 1223, 151-154, 1994
A;Title: Cloning and expression of a cDNA encoding bovine muscarinic acetylcholine m3
A;Reference number: 847572; MUID:94339178; PMID:8061048
A;Recession: 847572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   280 PVHPTGSSRSCSSYELQQQSMKRSARRKYGRCHFWFTTKSWKPSAEQMDQDHSSSDSWNN 339
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muscarinic acetylcholine receptor M2, glandular - pig

muscarinic acetylcholine receptor III

s) Alternate names: muscarinic acetylcholine receptor III

c) Species: Sus acrofa domestica domestic pig)

C) Dates: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004

C, Accession: S01114

R,Akiba, I.; Kubo, T.; Maeda, A.; Bujo, H.; Nakai, J.; Mishina, M.; Numa, S.

PRBS Lett. 235, 257-261, 1988
                                                                                                                                                                                                                                                                                                                                          NLAISDFFVGVISIPLYIPHTLFN-WNPGSGICMFWLITDYLLCTASVYSIVLISYDRYQ
                                                                                                                                                                                                                                                                                                                                                                                                        SLACADLIIGVISMNLFTTYIIMNRWALGNLACDLWLSIDYVASNASVANLLVISFDRYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLPLSFKEATLAKRFALKTRSQITKRKRMSLIKEKKAAQTLSAILLAFIITWTPYNIMVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVSNAVRYRAQHTGILKIVAQMVAV-WILAFLVNGPMILASDSW-----KNSTNTEECEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --IATSSRGTGHSRRTGLACRT----SLPG------LKEPAASLHSE
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                                                                                                                                                                                                                                                                                                                        1 MSESNGTDVLPLTAQ-----VPLAFLMSLLAFAITIGNAVVILAFVADRNLRHRSNYFFL
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                                                                                                                                                                                                                                                   20.1%; Score 410.5, -27; 24.8%; Pred. No. 4.2e-27; ....tive 78; Mismatches 159; Indels 175; ....tive 78; Mismatches 159; Indels 175;
                                                                                                                                                             A,Molecule type: mRNÅ
A,Residues: 1-590 «LEE»
A,Cross-references: UNIPROT:P41984; EM
C,Superfamily: Vertebrate rhodopsin
C,Keywords: neurotransmitter receptor
                                                                                                                                                                                                                                                                                         Matches 136; Conservative
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A;Title: Primary structure of porcine muscarinic acetylcholine receptor III and antagonis A;Reference number: 801114; MUID:88296835; PMID:3402600
A;Accession: 801114
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-590 <AKI>
A;Cross-references: UNIPROT:PI1483; EMBL:X12712; NID:g1861; PIDN:CAA31215.1; PID:g1862
A;Cross-references: UNIPROT:PI1483; EMBL:X12712; NID:g1861; PIDN:CAA31215.1; PID:g1862
C;Superfamily: vertebrate rhodopsin
C;Reywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmen C;Reywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmen #status predicted <TM1>
F;105-125/Domain: transmembrane #status predicted <TM2>
F;185-207/Domain: transmembrane #status predicted <TM3>
F;181-222/Domain: transmembrane #status predicted <TM5>
F;231-252/Domain: transmembrane #status predicted <TM5>
F;493-513/Domain: transmembrane #status predicted <TM5>
F;528-546/Domain: transmembrane #status predicted <TM5>
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muscarinic acetylcholine receptor M4 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: 13-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: A29476
R;Braun, T.; Schofield, P.R.; Shivers, B.D.; Pritchett, D.B.; Seeburg, P.H.
Biochem. Biophys. Res. Commun. 149, 125-132, 1987
A;Title: A novel subtype of muscarinic receptor identified by homology screening.
A;Reference number: A29476; MUID:88077068; PMID:3120722
A;Accession: A29476
A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.0%; Score 408.5; DB 2; Length 590; 24.7%; Pred. No. 6.2e-27; Live 79; Mismatches 158; Indels 175;
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A41632
histamine H1 receptor - bovine
                                                                                                                                                Best Local Similarity ....
Matches 131; Conservative
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Best Local S:
Matches 123,
                                                                                                                                                                                                                                                                                                                                                                           116
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A;Residues: 1-589 <BRA>
A;Cross-references: UNIPNCT:P08483; GB:M18088; NID:g202657; PIDN:AAA40659.1; PID:g202656
A;Experimental source: brain
C;Superfamily: vertebrate rhodopsin
C;Superfamily: reansmembrane #status predicted <TM1>
F;7-90,Domain: transmembrane #status predicted <TM3>
F;142-163/Domain: transmembrane #status predicted <TM4>
F;230-251/Domain: transmembrane #status predicted <TM6>
F;230-251/Domain: transmembrane #status predicted <TM6>
F;227-545/Domain: transmembrane #status predicted <TM6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Molecule type: DNA
A;Residues: 1-590 <PER>
A;Residues: 1-590 <PER>
A;Residues: 1-590 <PER>
A;Cross-references: UNIPROT: P20309; EMBL: X15266; NID: 932323; PIDN: CAA33337.1; PID: 932324
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transme
F;68-95/Domain: transmembrane #status predicted <TMI>
F;105-131/Domain: transmembrane #status predicted <TMI>
F;143-164/Domain: transmembrane #status predicted <TMI>
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C;Species: Homo sapiens (man)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S10128
R;Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, EMBO J. 6, 3923-3929, 1987
A;Title: Distinct primary structures, ligand-binding properties and tissue-specific eA;Reference number: S04326; WUID:88166632; PMID:3443095
                                                                                                                                                                                                                                                                                                                 17;
                                                                                                                                                                                                                                                                                                                                                                                              110
                                                                                                                                                                                                                                                                                                                                                                                                                                  59 ISDFFVGVISIPLYIPHTLFN-WNPGSGICMFWLITDYLLCTASVYSIVLISYDRYQSVS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CADLIIGVISMNLFTTYIIMNRWALGNLACDLWLSIDYVASNASVMNLLVISFDRYFSIT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAVRYRAQHTGILKIVAQMVAV-WILAFLVNGPMILASDSW----KNSTNTEECEPGFV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171 RPLTYRAKRT--TKRAGVMIGLAWVISFVLWAPAİL---FWQYFVGKRTVPPGEČFIQFL 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTGSSRSCSSYELQQQGVKRSSRRKYGRCHFWFTTKSWKPSAEQMDQDHSSSDSWNNNDA 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |: |: |: | : | ASLENDIGSETRALYSIVLKLPGHSSILNSTKLPSSDNLOVSNEDLGTVDVE 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----IAFKVGS 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNAHKLØAQKSMGDGDNCQKDFTKLPIQLESAVDTGKTSDTNSSADKTTATLPLSFKEAT 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----FCRSESPVLHQREHVELLRGRKLARSLAVLLSAFAICWAPYCLFTIVLSTYRRGER 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         337 PKSIWYSIAFWLQWFNSLINPFLYPLCHRRFQKAFWKIL---CVTKQPAPSQTQSVSS 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNGTDVLPLTAQ-----VPLAFLMSLLAFAITIGNAVVILAFVADRNLRHRSNYFFLNLA
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                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                       DB 2; Length 589;
                                                                                                                                                                                                                                                                   19.9%; Score 407.5; DB 2; Length 24.5%; Pred. No. 7.5e-27; ive 83; Mismatches 162; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --GSLSRCPSH----AGFIATSSRGTG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TEWYILAITAFLEFLLPVSLVVYFSVQIYWSLWKR--
                                                                                                                                                                                                                                                                                      Best Local Similarity 24.5
Matches 132; Conservative
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Cross-references: UNIPROT: P30546; GB: D10197; GB: D90430; NID: g217569; PIDN: BAA01045.1;
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R;Yamashite, M.; Fukui, H.; Sugama, K.; Horio, Y.; Ito, S.; Mizuguchi, H.; Wada, Proc. Natl. Acad. Sci. U.S.A. 88, 11515-11519, 1991
A;Title: Expression cloning of a cDNA encoding the bovine histamine H-1 receptor. A;Reference number: A41632; MUID:92107981; PMID:1722337
A;Accession: A41632
A;Status: preliminary
A;Molecule type: mRNA
                                                                                                                                                                                                                                                               19;
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                                                                                                                                                                                                                                                                                                                                                                                         109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSNAVRYRAQHTGILKIVAQMVAV-WILAFLVNGPMILASDSW-----KNSTNTEECEPG 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281 VHPTGSSRSCSSYELQQQSMKRSNRRKYGRCHFWFTTKSWKPSSEQMDQDHSSSDSWNNN 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DAAASLENSASSDEEDIGSETRAIYSIVLKLPGHSTILNSTKLPSSDNLQVPEEELGMVD 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               401 LERKADKLQAQKSVDDGGSFPKSFSKLPIQLESAVDTAKTSDVNSSVGKSTATLPLSFKE 460
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                                                                                                                                                                                                                                                                                                                             98
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                                                                                                                                                                                                                                                                                                                             SESNGTDVLPLTAQ-----VPLAFLMSLLAFAITIGNAVVILAFVADRNLRHRSNYFFLN
                                                                                                                                                                                                                                                                                                                                                                  | :|| :| :| :: |::| :| || SPPGTTDDPLGGHTVWQVVFIAFLTGILALVTIIGNILVIVSFKVNKQLKTVNNYFLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAISDFFVGVISIPLYIPHTLFN-WNPGSGICMFWLITDYLLCTASVYSIVLISYDRYQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  461 ATLAKRFALKTRSQITKRKRMSLVKEKKAAQTLSAILLAFIITWTPYNIMVLV-NTFCDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CIPKTFW-NLGYWLCYINSTVNPVCXALCNKTFRTTFKM1LLCQCDKKKRRKQQYQQRQS
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C;Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSESNGTDVLPLTAQVPLAFLMSLLAFAITIG-NAVVILAFVADRNLRHRSNYFFLNLAI
                                                                                                                                    #status predicted
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                                                                                                                                                                                                                                                               161;
                                                                                                                                                                                                Length 590;
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A, Cross-references: UNIROT: P30546; GB: D10197; GB: D90430; NID
A, Cross-references: UNIROT: P4060psin
C, Superfamily: vertebrate rhodopsin
C, Reywords: G protein-coupled receptor; transmembrane protein
F;185-207/Domain: transmembrane #status predicted <TM4>
F;231-252/Domain: transmembrane #status predicted <TM5>
F;493-513/Domain: transmembrane #status predicted <TM6>
F;525-546/Domain: transmembrane #status predicted <TM6>
F;55,6,15,41/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                               85; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.6%; Score 401.5; DB 2; 24.8%; Pred. No. 2e-26;
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                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FVTEWYILAITAFLEFLLPVSLVVYFSVQIYWSLWKR-
                                                                                                                                                                                                                                 Pred. No. 1.6e-26
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                                                                                                                                                                                            19.7%; Score 403.5; 24.3%; Pred. No. 1.6
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muscarinic acetylcholine receptor M3 - rat

G.Species: Rattus norvegicus (Norway rat)

C.Species: Rattus norvegicus (Norway rat)

C.Species: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004

C.Species: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004

C.Species: Association: B94518 B37121; B29514

R.Bonner, T.I.

Submitted to GenBank, July 1987

A.Rocession: B94518

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 YYLLSLACADLIIGIFSMNLYTTYILMGRWVLGSLACDLWLALDYVASNASVMNLLVISF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 KGPDPNLSHQMTKRKRMVLVKERKAAQTLSAILLAPIIIWTPYNIMVLV-STFCDKCVPV 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 YFFLNLAISDFFVGVISIPLYIPHTLF-NWNPGSGICMFWLITDYLLCTASVYSIVLISY 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DRYQSVSNAVRYRAQHT----GILKIVAQMVAVWILAFLVNGPMILASDSW-----KNST 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297 EQVITC-SSYPSSEDEAKPITDPVPQMVYKSEAKESP-GKESNTQETKETVVNTRIENSD 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----SESP-- 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 YDTPKYPLSPAAHRLKSOKCVAYKFRLVVKADGTQETNNGCRKVKIMPCSFPVSKDPST 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----VLHO---REHVELLRGRKLARSLAVLLSAFAICWAPYCLFTIVLSTYRRGERPK 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 STVNGT---PVNHQALERHGLWEVITIAVVTAVVSLMTIVGNVLVMISFKVNSQLKTVNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 DRYFSITRPLTYRAKRTPKRAGIMIGLA-----WLVSFILWAPAILC---WQYLVGKRTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 AKKREPAQRILLRSFFSCPRPSLAQRERNQASW-SSSRRSTSTTGKTTQATDLSADWEKA
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F;443-463/Domain: transmembrane #status predicted <TM6>
F;478-496/Domain: transmembrane #status predicted <TM7>
F;7,12/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                            19.6%; Score 401; DB 2; Length 531;
25.9%; Pred. No. 2.4e-26;
tive 84; Mismatches 137; Indels 166;
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C;Superfamily: vertebrate rhodopsin
C;Rywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho F;29-52/Domain: transmembrane #status predicted <TM1>
F;66-86/Domain: transmembrane #status predicted <TM2>
F;104-125/Domain: transmembrane #status predicted <TM4>
F;104-123/Domain: transmembrane #status predicted <TM4>
F;191-213/Domain: transmembrane #status predicted <TM5>
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A; Reaidues: 1-531 <BON>
A; Reaidues: 1-531 <BON>
A; Cross-references: UNIPROT: P08911
B; Lidao, C.F., Themmen, A.P.N.; Joho, R.; Barberis, C.; Birnbaumer, M.; Birnbaumer, L.
J. Biol. Chem. 264, 7328-7337, 1989
A; Title: Molecular cloning and expression of a fifth muscarinic acetylcholine receptor.
A; Reference number: A33354; MUID: 89214170; PMID: 2540186
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SDFFVGVISIPLYIPHTLFN-WNPGSGICMFWLITDYLLCTASVYSIVLISYDRYQSVSN 118
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Cispecies: Rattus norregicus (Norway rat)
Cispecies: Rattus norregicus (Norway rat)
Cipaces al-Mar-1992 #sequence revision 31-Mar-1992 #text_change 09-Jul-2004
CiAccession: JT0531, A33354; C37121
Ribonner, T.I.; Young, A.C.; Brann, M.R.; Buckley, N.J.
Neuron 1, 403-410, 1988
A;Title: Cloning and expression of the human and rat m5 muscarinic acetylchc A;Reference number: JT0530; MUID:90166521; PMID:3272174
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                                                                                                                                                                                                            119 AVRYRAQHTGILKIVAQMVAVWILAFLVNGPMILASDSWKN-----STNTEECEPGFVT
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A;Title: Genomic cloning, heterologous expression and pharmacological characterization of A;Reference number: JC2035; MUID:94107375; PMID:8280179
A;Accession: JC2035
                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-487 <DEB>
A;Cross-references: GB:X76786; NID:g442517; PIDN:CAA54182.1; PID:g442518
A;Moguilevsky, N.; Varsalona, F.; Noyer, M.; Gillard, M.; Guillaume, J.P.; Garcia, L.; S;
Eur. J. Biochem. 224, 489-495, 1994
A;Title: Stable expression of human H(1)-histamine-receptor cDNA in Chinese hamster ovary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-487 <MOG>
A;Cross-references: EMBL:234897; NID:g510295; PIDN:CAA84380.1; PID:g510296
C;Comment: This receptor mediates the increase in capillary permeability through immune-1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 3p21-3p14
C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate rhodopsin
F; 30-49/Domain: transmembrane #status predicted <TM1>
F; 64-83/Domain: transmembrane #status predicted <TM2>
F; 100-121/Domain: transmembrane #status predicted <TM3>
F; 100-209/Domain: transmembrane #status predicted <TM5>
F; 130-139/Domain: transmembrane #status predicted <TM6>
F; 140-148/Domain: transmembrane #status predicted <TM6>
F; 1419-148/Domain: transmembrane #status predicted <TM6>
F; 1419-148/Domain: transmembrane #status predicted <TM6>
F; 1410-148/Domain: transmembrane #status predicted <TM7>
F; 1410-148/Domain: transmembrane #status predicted <TM6>
F; 1410-148/Domain: transmembrane #status predicted <TM6>
F; 1410-148/Domain: transmembrane #status predicted <TM6>
F; 1410-148/Domain: transmembrane #status predicted <TM7>
F; 1410-148/Domain: transmembrane #status predicted <TM6>
F; 1410-142,390,478/Binding site: phosphate (Sar) (covalent) (by protein kinase C) #status F; 1410,142,390,478/Binding site: phosphate (Thr) (covalent) (by protein kinase C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 250 KPGKESPWEVLKRKPKDAGGGSVLKSPSQTPKEMKSPVVFSQEDDREVDKLYCPPLDIVH 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 FKVMTAIINFYLPTLLMLWFYAKİYKAVRQHCQHRELINRSLPSFSEIKLRPENPKGDAK 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GFIA 220
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                                                                                                                                                                                                                                                                                                                                                                                          localisation of the gene.
A;Reference number: S48144; MUID:95010026; PMID:7925364
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               Biophys. Res. Commun. 197, 1601-1608, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: GDB:303929; OMIM:600167
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Best Local Similarity 24.8%
Matches 120; Conservative
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-487 <FUK>
A;Cross-references: UNIPROT: P35367; DDBJ:D14436; NID: 9506335; PIDN: BAA03319.1; PID: 95382
R;De Backer, M.D.; Gommeren, W.; Moereels, H.; Nobels, G.; Van Gompel, P.; Leysen, J.E.;
                                                                                                                               receptor; transme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17;
A;Molecule type: protein
A;Residues: 104-166 <KUR>
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter recepto
E;67-90/Domain: transmembrane #status predicted <TM1>
F;104-1124/Domain: transmembrane #status predicted <TM2>
F;184-206/Domain: transmembrane #status predicted <TM3>
F;230-251/Domain: transmembrane #status predicted <TM5>
F;230-251/Domain: transmembrane #status predicted <TM5>
F;482-512/Domain: transmembrane #status predicted <TM5>
F;527-545/Domain: transmembrane #status predicted <TM7>
F;6,15,41,48,52/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 ISDPFVGVISIPLYIPHTLFN-WNPGSGICMFWLITDYLLCTASVYSIVLISYDRYQSVS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.4%; Score 397.5; DB 2; Length 589; 24.2%; Pred. No. 5.3e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84; Mismatches 159; Indels
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Matches 131; Conservative
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369

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C;Species: Mus musculus (house mouse)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A42688; S2219, N.; Boschert, U.; Plassat, J.L.; Hen, R.
Proc. Natl. Acad. Sci. U.S.A. 89, 3020-3024, 1992
A;Title: Mouse SHTIB serotonin receptor: cloning, functional expression, and localization A;Reference number: A42688; MUID:92212959; PMID:1557407
A;Reference number: A42688
A;Status: preliminary
                                                                                                                                                                                                                                                                                   Risaudou, F.
submitted to the BMBL Data Library, January 1992
A;Reference number: $22191
A;Accession: $22191
A;Accession: $22191
A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-366 <5AU>A;Residues: 1-366 <5AU>A;Residues: 1-366 <5AU
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rcoupled receptor; glycoprotein; neurotransmitter receptor; transmen
                                                                                                                                                                                                                     A;Residues: 1-1386 <MAR>
A;Residues: 1-386 <MAR>
A;Cross-references: UNIPROT:P28334; GB:M85151; NID:g191529; PIDN:AAA83221.1; PID:g191530
A;Note: sequence extracted from NCBI backbone (NCBIN:93807, NCBIP:93808)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 FYLPTLLIALYGRIYVBARSR-ILKQTPNKTG------KRLTRAQLITDSPGST 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261 SSVTSINSRAPDVPSE-----SGSPV--YVNQVKVRVSDALLEKKKLMAARERKAT 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245 EPAASLHSESPRGKSSLLVSLRTHMSGSIIAFKVGSFCRSESPVLHQREHVELLRGRKLA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSLAVLLSAFAICWAPYCLFTIVLSTYRRGERPKSIWYSIAF-----WLQWFNSLINPFL 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310 KTLGIILGAPIVCWLPPFIISLVMPICK----DACWFHMAIPDFFNWLGYLNSLINPII 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 SIPLYIPHTLF-NWNPGSGICMFWLITDYLLCTASVYSIVLISYDRYQSVSNAVRYRAQH 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 TGILKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTEECEPGFVTEWYIL--AITAFLE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 FLLPVSLVVYFSVQIYWSLWKRGSLSRCPSHAGFIATSSRGTGHSRRTGLACRTSLPGLK 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 DSIALPWKVLLVALLALITLATTLSNAFVIATVYRTRKIHTPANYLIASLAVTDLLVSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 TP-KRAAIMIVLVWVFSISISLPPFF----WRQAKAEEEMLDCFVNTDHVLYTVYSTVGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 DVLPLTAQVPLAFLMSLLAFAITIGNAVVILAFVADRNLRHRSNYFFLNLAISDFFVGVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.1%; Score 390.5; DB 2; Length 3 ilarity 27.4%; Pred. No. 1.3e-25; Conservative 73; Mismatches 159; Indels
  Alternate names: 5-hydroxytryptamine 1B receptor (5HTR-1B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360 YPLCHRRFQKAFWKIL 375
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365 YTMSNEDFKQAFHKLI 380
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Best Local Similarity
Matches 103; Conserva
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                                                                                                                                                                                                                                                                                         RiBonner, T.I.; Young, A.C.; Brann, M.R.; Buckley, N.J.
Murcon I, 403-410, 1988
Alitle: Cloning and expression of the human and rat m5 muscarinic acetylcholine receptor A; Reference number: JT0530; MUID:90166521; PMID:3272174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHAGFI------LACRT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLPGLKE---PAA-----SLHSESPRGKSS------LLV 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AISDFFVGVISIPLYIPHTLF-NWNPGSGICMFWLITDYLLCTASVYSIVLISYDRYQSV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNAVRYRAQHT----GILKIVAQMVAVWILAFLVNGPMILASDSW-----KNSTNTEECE 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGFVTEWYILAITAFLEFLLPVSLVVYFSVQIYWSLWKR------GSLS-----RCP 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 IQFLSEPTITFGTAIAAFYIPVSVMTILYCRIYRETEKRTKDLADLQGSDSVTKAEKRKP 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 AHRALFRSCLRCPRPTLAQRERNQASWSSSRRSTSTTGKPSQATGPSANWAKAEQLTTCS 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q----REHVELLRGRKLARSLAVLLSAFAICWAPYCLFTIVLSTYRRGERPKSIWYSIAFW 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72
                                                                                                                                     Species: Homo sapiens (man)
Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NGTDV--LPLTAQ-----VPLAFLMSLLAFAITIGNAVVILAFVADRNLRHRSNYFFLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.3%; Score 395; DB 2; Length 532;
26.3%; Pred. No. 7.8e-26;
tive 79; Mismatches 145; Indels 154;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264 SLRTH--MSGSIIAFKVGSFCRSES-----
                                                                                                                      muscarinic acetylcholine receptor M5 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 135; Conservative
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A4268
Serotonin receptor 1B - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sest Local Similarity
:||
KRIL 483
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DB 2; Length 386;

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A24325
muscarinic acetylcholine receptor - pig
muscarinic acetylcholine receptor - pig
c.Species: Sus scrofa domestic pig)
C.Species: Sus scrofa domestic pig)
C.Species: Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 09-Jul-2004
C.Species: Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 09-Jul-2004
C.Species: Make 125
Nature 323, 411-416, 1986
A;Rithe: Cloning, sequencing and expression of complementary DNA encoding the muscarinic A;Reference number: A24325; MUID:87014801; PMID:3762692
A;Rocession: A24325
A;Molecule type: mRNA
A;Residues: 1-460 «KUB>
A;Ross-references: UNIPROT:P04761; GB:X04413; NID:g1863; PIDN:CAA28003.1; PID:g1866
C;Superfamily: vertebrate rhodopsin
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cds: G protein-coupled receptor; glycoprotein; r Domain: transmembrane #status predicted <tm1> 11/Domain: transmembrane #status predicted <tm2> 11/Domain: transmembrane #status predicted <tm3> 18/Domain: transmembrane #status predicted <tm3> 19/Domain: transmembrane #status predicted <tm3> 19/Domain: transmembrane #status predicted <tm5> 11/Domain: transmembrane #status predicted <tm5></tm5></tm5></tm3></tm3></tm3></tm2></tm1>	
Query Match  Query Match  Best Local Similarity 27.5%; Pred. No. 1.9e-25;  Matches 119; Conservative 80; Mismatches 161; Indels 73; Gaps 17;	Db 273 FLSEPLITFGTALAAFYLPVTIMSI-LYWRIYKE-TEKRTKELAGLQASGSEAETAR 327 Qy 226TGHSRTG
OY 5 NGTDVLPLTAQVPLAFLMSLLAFAITIGNAVVILAFVADRNLRHRSNYFFLNLAISD 61	Db 328 FVHQTGSRELGSYELQRQSTKRSSRRKYRRCHFWLTWKSPNTDQGDQEHSSSDSWNN 387 Qy 244 KEPAASLHSESPRGKSSLLVSLRTHMSGSIIAFKV 278
Qy 62 FFVGVISIPLYIPHTLF-NWNPGSGIGWFWLITDYLLCTASVYSIVLISYDRYQSVSNAV 120 :	Db 388 NDAAASLENSASSDEEDITAETRAIYSIVLKLPGH-SAILNSTKLPSSEDLNESADELQK 446 Qy 279
Qy 121 RYRAQHTGILKIVAQMVAV-WILAFLVNGPMILASDSWKNSTNTEECEPGFVTEW 174	Db 447 SDTDSQEKKPKKLQPPKSIQDGGSFQKSFSKLPIQPGSAETATASDGISSVTKTSAALPL 506 Qy 289LHQREHVELLRGRKLARSLAVLLSAFAICWAPYCLFTIVLST 330
Qy 175 YILAITAFLEFLLPVSLVVYFSVQIYWSLWKRGSLSRCPSHAGFIATSSR 224	DD 507 SFKEATLAKKPALKTRSQITKRKRMSLIKEKKAAQTLSAILPAPIITWTPYNIMVLV-NT 565 Qy 331 YRRGERPKSIMYSIAPWLQWFNSLINPFLYPLCHRRFQKAFWKILCVTKQPAPSQTQ 387
OY 225GTGHSRTGLACR-TSLPGLKEPAA-SLHSESPRGKSSLLVSLRTHWSGSIIAF 276	566
277 KVGSF-CRSESPV	UY 500 503 571 Db 624 QRQS 627
Db 303 KMPMVDPEAQAPAKQPPRSSPNTVKRPTRKGRERAGKGQKPRGKEQLAKRKTFSLVKEKK 362	RESULT 14
QY 303 LARSLAVLLSAFAICWAPYCLFTIVLSTYRRGERPKSIWYSIAFWLQWFNSLINPFLYPL 362	
Qy       363 CHRRPQKAFWKIL 375         Db       421 CNKAFRDTFRLLL 433	C.Date: 31-Dec-1990 #sequence revision 31-Dec-1990 #text_change 09-Jul-2004 C;Accession: 809508; S06327; \$04326 R;Chapman, C.G.; Browne, M.J. Nucleic Acids Res. 18, 2191, 1990
	A.Title: Isolation of the human ml (Hml) muscarinic acetylcholine receptor gene by PCR an A;Accession: S09508; MUID:90245684; PMID:2336407 A;Accession: S09508 A;Status: nucleic acid sequence not shown; translation not shown
<pre>le receptor, M3 isoform - chicken is (chicken) squence_revision 11-Nov-1994 #text_change 09-Jul-2004 J.B.</pre>	A; Molecule type: DNA A; Residues: 1.460 CCHA> A; Cross-references: UNIFROT: P11229; EMBL: X52068; NID: 934450; PIDN: CAA36291.1; PID: 934451 A; Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1990 R; Allard, W.J.; Sigal, I.S.; Dixon, R.A.F.
323-25829, 1994 Starinic acetylcholine receptor is expressed in chick atrium and S019; MUID:95014393; PMID:7929287	Nucleic Acids Res. 15, 10604, 1987.  Nucleic Acids Res. 15, 10604, 1987.  A.Fitle: Sequence of the gene encoding the human M1 muscarinic acetylcholine receptor.  A.Reference number: S06327, MUID:88096607; PMID:3697105  A.Accession: S06327
A;STRIUB: preliminary A;Molecule type: mRNA A;Residues: 1-639 cGAD> A;Cross-references: UNIPROT:P49578; GB:L10617; NID:g530097; PIDN:AAA65961.1; PID:g530098 C;Superfamily: vertebrate rhodopsin C;Keywords: neurotransmitter receptor	A;Molectule type: DNA A;Residues: 1-460 <alll> A;Residues: 1-460 <alll> A;Cross-references: GB:Y00508; GB:W35128; NID:g297405; PIDN:CAA68560.1; PID:g297406 R;Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J EMBO J. 6, 3923-3929, 1987 A;Tille: Distinct primary extructures, ligand-binding properties and tissue-specific expressible to be a perference outside to be a perference outside.</alll></alll>
Query Match  Query Match  Best Local Similarity 24.6%; Pred. No. 3.1e-25;  Matches 134; Conservative 89; Mismatches 153; Indels 168; Gaps 21;	A.Accession: SO4326 A.Accession: SO4326 A.Molecule type: DNA A.Residues: 1.172, W.Y.174-460 < PER>
Qy 2 SESNGTDVLPLTAQVPLAFLMSLLAFAITIGNAVVILAFVADRNLRHRSNYFFLN 56	C;Superfamily: vertebrate rhodopsin C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphop F:25-50/Domain: transmembrane #status predicted <tml> F;62-93/Domain: transmembrane #status predicted <tm2> F;100-121/Domain: transmembrane #status predicted <tm3></tm3></tm2></tml>

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C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C/Accession: T18863
R/Baynes, C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 YILAITAFLEFLLPVSLVVYFSVQIYWSLWKR-----GSL--SRCPSHAGFIATSSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGTDVLPLTAQVPLAFL---MSLLAFAITIGNAVVILAFVADRNLRHRSNYFFLNLAISD
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Introns: 54/3; 124/1; 159/2; 184/3; 218/2; 256/1; 313/3; 348/3; 406/3;
Superfamily: octopamine receptor type I
F:142-168/Domain: transmembrane #status predicted <TM4>
F:187-209/Domain: transmembrane #status predicted <TM5>
F:187-209/Domain: transmembrane #status predicted <TM6>
F:167-420/Domain: transmembrane #status predicted <TM7>
F:20.12/8inding site: carbohydrate (Asn) (covalent) #status predicted
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25.8%; Pred. No. 2.9e-25;
tive 84; Mismatches 161; Indels 100;
                                                                                                                                                                                                                                                                                                                                                                           73;
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                                                                                                                                                                                                                                                                             ; Score 388.5; DB 2; Length 4; Pred. No. 2.4e-25; 80; Mismatches 161; Indels
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Best Local Similarity 27.5%;
Matches 119; Conservative 80
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Matches 120; Conservative
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| SBI FSFCWLPFFVAYVIRPFCETCKLHAKATPPLTIYYRQNKHAIFFIRFIFGLHDRLANLSRK 440
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|| | : : || : | || | SDLAVAIFVMPLHAQOFSFLLCSALFLFSGKWLLGVTVCQFFTTADILLCTSSIL
                                                                                                                                          104 SIVLISYDRYQSVSNAVRYRAQHTGILKIVA-QMVAVWILAFLVNGPMILASDSWKNSTN
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BXF2g781C0629_x1 781 (synonym: hlcc4) Homo sapiens cDNA clone
DXF2g781C0629_5', mRNA sequence.
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKZPZ); Email 8. Wiemann@dKt2- heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No 81 sequence available.
This clone (DKEZp781C0629) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin- Charlottenburg, GERWANY; Email: clone@rzpd.de.
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EST (Lauber,J., Bahr,A., Mewes,H.W., Weil,B., Amid,C., et al.) Unpublished (2003)
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-DEST_CPMT=fastap -SUPFIX=rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -GTART=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSEPILOK=10 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THRRANS=1 -XGAPDP=10 -XGAPEXT=0.5 -FGAPOP=6
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Bukaryota; Wetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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L Office of Cancer Genomics

National Cancer Genomics

National Cancer Institute / NIH

Bldg: 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.inih.gov

Tissue Procurement: GPCR Consortium
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Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-remail.nih.gov

Tissue Procurement: Guthrie cDNA Resource Center

CDNA Library Preparation: Guthrie cDNA Resource Center

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:

http://image.llnl.gov

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High quality sequence start: 2

High quality sequence stop: 328.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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AGENCOURT 30842625 NIH MGC 146 Homo sapiens CDNA clone
IMAGE:7389774 5', mRNA sequence.
CO955034
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/clone_lib="NIH_MGC_146"
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/db_xref="taxon:9606"
/clone="IMAGE:7389774"
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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.

En 1 (bases 1 to 73)

NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lupublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 RauloA07 Betheada, MD 20892

Email: Ggapbs-r@mail.nih.gov

Tissue Procurement: GPCR Consortium

CDNA Library Preparation: GPCR Consortium

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
/note="Vector: pcDNA3.1; Site 1: multiple; Site_2: multiple; ORF's were PCR-amplified (from IMAGE clones or from commercially available cDNA libraries) and cloned by the Guthrie cDNA Resource Center (www.guthrie.org/cDNA) into pcDNA3.1. For specific information on cloning sites (which vary by clone), please refer to the Guthrie website, using the Guthrie ID given in the file ftp://image.lnl.gov.image.rearrayed_plates/IRBF.preSV.dat a. Note: this is a NIH_MGC Library."
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AGENCOURT 14740187 NIH_MGC_145 Homo sapiens cDNA clone IMAGE:6971899 5', mRNA sequence.
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Conservative:
Mismatches:
Indels:
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23.67%
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Best Local Similarity:
Query Match:
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AY400782 17-DBC-2003 Homo sapiens CHRM3 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
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1 (bases 1 to 1773)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., And, Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Sheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
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    1773
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

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/gene="CHRM3"
/locus_tag="HCM0672"
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DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information (found through the I.M.A.G.E. Consortium/LLNL at: http://mage.lln.gov
Plate: IRBIC2 row: b column: 06
High quality sequence stop: 610.
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	rat) ta; Craniata; Vertebrata; Bu ia; Sciurognathi; Muridae; M	One Amean Center Drive, Thousand Oaks, CA 91320-1799, USA Tal: 805 447-4881 Plate: 00001 row: d column: 6.  EATURES Location/Qualifiers Location/Qualifiers    0.572   0.572   0.572   0.572   0.572   0.572   0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016  0.572   0.500-1016	Alignment Scores: 5.93e-29 Length: 672  Pred. No.: 401.00 Matches: 80  Score: 401.00 Matches: 22  Best Local Similarity: 56.34 Mismatches: 36  Query Match: 19.614 Indels: 4  DB: 6 Gaps: 2	18 LeualaPheLeumetSerLeu 18 LeualaPheLeumetSerLeu 227 CTGGCTGCGCTCATGGCGCTG	Oy 38 LeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
LeuLeuCysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSer  :::::::::::::::::::::::::::::::::::	SerLeuvalvalTyrPheServalGln	237 ArgThrSer	268 sMetSerGlySerIle	CTCCAAGCTTCCCATCCAGCTAGAGTCAGCCGTGGACACAGCTAAGACTTCTGACGTCAA 13	1332 CTCCTCAGTGGGTAAGAGCACGGCCACTCTGTCCTTCAAGGAAGCCACTCTGGC 1391 289

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S clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Tolach, M., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Adams, M.D. and Cargill, M.

Direct Submission

L Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers

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Clark, A.G.; Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Aderniers, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, White, T.J., Sninsky, J.J., Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              694 GCTGTCAGTTACCGAGCTCAGCAGAGTAACAGCCGGCATGCAGTCTTGAAAATGACCATG 753
                                                                                                                                                                                                                                                                                                                                                                                                                             SerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPhe--- 78
                                                                                                                                                                                                                                                                                                    40 PheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlalle
                                                                                                                                                                                                                     79 AsnTrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCys
                                                               -- LeuThrAlaGlnValProLeuAla
                                                                                                                     334 riccagradadadadaacarriccegagaraccaaacrrrrrecradacacgierrecradeer
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Mus musculus CHRM3 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
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AY400784.1 GI:39756773
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                                                            4 SerAsnGlyThrAspValLeuPro----
   US-10-626-126-9 (1-391) x CD326085 (1-853)
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AGENCOURT_14163426 NICHD_XGC_Eyel Xenopus laevis cDNA clone
AGENCOURT_549081 5', mRNA sequence.
                                                            116
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                                                                                                                                                                                                                                                                                                    137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
                                                                                                                                                                                                                                                                                                                                                                 637
107 ACCGGCCGTTGGACCTTCGGCCGGGCCTCTGCAAGCTGTGGCTGGTGGTAGACTACCTA 466
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/lab.host="DH10B (phage-resistant)"
/clone lib="NICHD XGC Ept."
/note="Grgan: eye; Vector: pCMV-SPORT6; Site 1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection
(XGC) library."
                                                                                                                                                                                                                        LeuCysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerVal
                                                                                         587 GCACTGGTGTGGGTGCTTCCTGCTGTATGGGCCTGCCATCCTG-----AGT
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/organisme"Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:6949081"
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	Qy         273         273         273         273           Db         1215         TAAGCTTCAGGCCCAGAACAGTATGGATGACCGTGACAACTGTCAGAAGGACTTCTCCAA         1274           Qy         273	1275 GCTCCCCATCCAGTTAGAGTCTGCCGTGGACACAGCCAAGACCTCTGACACCAACTCCTC  274	Qy         281 - PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGl 300	Qy 320 oTyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIl 340	340 eTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTy     :::::	Oy 360 reconcupants and a procession of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control	RESULT 9 AK080950 LOCUS AK080950 AK080950 AK080950 DEFINITION Mus musculus 4 days neonate male adipose cDNA, RIKEN full-length enriched library, clone:B430217G05 product:MUSCARINIC ACETYLCHOLINE RECEPTOR M3 (MM3 MACHR), full insert sequence. VERSION AK080950 ACCESSION AK080950 ACCESSION AK080950 ACCESSION AK080950	S ISM CE RS	TITLE HIGH-EFILICATION TULTIFIER CONTROL COURNEL TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO THE HIGH-EFILICATION TO TH
Alignment Scores: 6.39e-28 Length: 1770 Score: 397.50 Matches: 136 Secret Similarity: 41.31\$ Mismatches: 160 Best Local Similarity: 25.42\$ Mismatches: 160 Ouery Match: 9.44\$ Indels: 155 DB: 9 Gaps: 18	4 SerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeu	AlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeu	59 lleSerAspPhePheValGlyVallleSerlleProLeuTyrlleProHisThrL :::	Db 391 AACGGTGGGGTCTGGGGAACTTAGCCTGTGACCTTGGCTTTCCATTGACTATGTGGCC 450  Qy 98 CysThralaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSer 117	AsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuLysIleVàlAlaGlnMetVal	Oy 138 AlaValTrpIleLeuAlaPheLeuValAsnGlyProMetileLeuAlaSerAspSer 156  11	172 ThrGluTrpTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuLeuProValSerLeu 172 ThrGluTrpTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuLeuProValSerLeu 172 ThrGluTrpTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuLeuProValSerLeu 173 AgradaCccaccaTcaccTTcGGCAcGGCGATCGCTGCCTTTTACATGCCTGTCACCTGTCATGCTGTCATGCTGTCATGCTGTCATGCTGTCATGCTGTCATGATATATAT	TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGly    :::	231 231 245 245 275 250

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ENFVHPTGSSRSCSSYELQQQCTKRSSRRKYGGCHFWFTTKSWKPSREQMDQDHSSSD
SWNNNDAASLENSASSDEEDIGSETRAIYSIVLKLPGHSTILNSTKLPSSDNLQVPD
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RRKQQYQQRQSVIFHKRVPEQAL"
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NYFLLSLACADLIIGVISMNLFTTYIIMNRWALGNLACDLWLSIDYVASNASVMNLLV
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ECFIQPLSEPTITFGTAIAAFYWPVTIMTILYWRIYKBTEKRTKELAGLQASGTEAEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 CysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSer 117
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                                    Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yondawe, K., Togawa, X., Izawa, M., Ohara, E., Watshiki, M., Yonda, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Sokazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="4 days neonate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 40, 563-573 (2002)

6 (bases 1 to 3171)
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RECEPTOR M3 (MM3 MACHR) (SWISSPROT|Q9ERZ3, evidence:
FASTY, 100%ID, 100%length, match=1767)
                                                                                                                                                                                                                                                                                                                                                                           the RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                       Punctional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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/db_xref="taxon:<u>1</u>0090"
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Dp 1	1579 TGGGCTACAGGCCTCTGGGACAGAGCGGAAGCAGAAACTTTGTCCACCCCACAGGCAG 1638	CRGANTON	
9 B	218 Phelle	REFERENCE AUTHORS TITLE	1 Carninci, P. ar High-efficienc
ò	231 gThrGlyLeuAlaÇyş 244	JOURNAL	Meth. Enzymol. 99279253
Db 1		PUBMED REFERENCE	10349636
È	245GluProAlaAlaSerLe 250	AUTHORS	Carninci, P., S Itoh, M., Konno
Db 1		TITLE	prepare full-1
ò	250 uHisSerGluserProArg 256	MEDLINE	Genome Kes. 10 20499374
Db 1	1819   GGAAAACTCTGCTTCTTCTGATGAAGAGGATATTGGCTCAGAGACCAGAGCCATCTATTC 1878	REFERENCE	
ò	257GlyLygSerSerLeuLeuValSerLeuArgThrHisMetSe 270	AUIHUKS	Konno, H., Akiy
Db 1	1879 CATTGTACTCAAGCTGCCGGGTCATAGCACCATCCTCAACTCTACCAAGCTACCCTCCTC 1938		Yamamoto, R., N
ò	270 rdlySerIle 273		Yoneda, Y., Ish
Db 1	1939 AGATAACCTGCAGGTGCCAGACAAGGACCTGGGGACTATGGATGTAGAGAAAATGCCCA 1998	TITLE	RIKEN integrat
ò	273 273	JOURNAL	Sequencing pig Genome Res. 10
Db 1	1999 TAAGCTTCAGGCCCAGAAGAGTATGGATGACCGTGACAACTGTCAGAAGGACTTCTCCAA 2058	PUBMED	11076861
ò	273 273	AUTHORS	The RIKEN Genc
Db 2	2059 GCTCCCCATCCAGTTAGAGTCTGCCGTGGACACAGCCAAGACCTCTGACACCAACTCCTC 2118	TITLE	Functional and
ò	274 280 116AlaPheLysValGlySer 280	REFERENCE	Nature 409, 65
0b 3	2119 GGTGGACAAGACCACGGCCGCTCTACCTGTCCTTCAAAGAAGCCACGCTGGCTAAGAG 2178	AUTHORS	Group Phase I
È	rgGluHisValGluLeu	TUME	of 60,770 full
Db 2	1179 GTTTGCTCTCAAGACCAGAAGTCACAAGGGGAAAAGGATGTCGCTCATCAAGGA 2238	REFERENCE	Nature 420, 5t 6 (bases 1 to
ò	300 yArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPr 320	ACIDORS	Fukuda, S., Fur
Dp 5	2239 GAAGAAAGGCCGCCCAGACACTCAGTGCCATCTTGCTGGCTTTCATCATCATGGACCCC 2298	•	Hori, F., Imota
ò	320 oTyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIl 340		Koya, S., Kurih
Db 2	- <del>b</del>		Okazaki, Y., Se
ò	AlaPheTrpLeuGlnTrpPheAsnSerLeu		Sogabe, Y., Tag
0p	11 ::::: :::::::::::::::::::::::::::::	Đ.	Muramatsu, M. &
ò	360 rProLeuCysHisArgPheGlnLysAlaPheTrpLysIleLeuCysVa 377	JOURNAL	Submitted (16-
Dp 5	2413 TGCCCTGTGCAACAAGAACATTCAGAACCACCTTCAAGATGCTTCTCTTATGCCAGTGTGA 2472		Exploration Reported Volvohama
ò	377 lThrLysGlnProAlaProSerGlnThrGlnSerValSerSer 391		Kanagawa 230-( IRL:http://ger
	2473 CAAGAGGAAGCGGCGCAAACAGCÁGTACCÁGCAGAGACAGTĆĆ 2515	COMMENT	Fax:81-45-503- CDNA library v
RESULT 10 AK032763 LOCUS	AK032763 2780 bp mRNA linear HTC 03-APR-2004		Encyclopedia I Genomic Sciend Division of Ex
DEFINITION	N Mus musculus 12 days embryo male wolffian duct includes surrounding region cDNA, RIKEN full-length enriched library, clone:6720430L06		prepare mouse Please visit o
ACCESSION			URL: nttp://ger URL: http://far

AK032763.1 GI:26328544 HTC; CAP trapper. Mus musculus (house mouse)

AK032763

ACCESSION VERSION KEYWORDS SOURCE

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Alzawa, K. Akimura, T., Arakawa, T., Bono, H., Carninci, P., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., K., Haye, M., Hanado, M., Hiraoka, T., Hirozane, T., Himotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kurihara, C., Marsuyama, T., Miyazaki, M., Munata, M., Noshi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sasito, R., Shibata, K., Shakawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
                                                                                                                                                                                                                                                                                                                                                  Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., no,H., Oƙazaki,Y., Muramatsu,M. and Hayashizaki,Y. n and subtraction of cap-trapper-selected cDNAs to-length cDNA libraries for rapid discovery of new genes 10 (10), 1617-1630 (2000)
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Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
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563-573 (2002)
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Sciurognathi, Muridae, Murinae, Mus
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ncy full-length cDNA cloning
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AK047070 2831 bp mRNA linear HTC 03-APR-2004 Mus musculus 10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:B930016C09 product:HISTAMINE RECEPTOR H1, full insert sequence.

AK047070 GI:26338557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       988 ATGCAGACACAGCCTGTGCCTGAGGGAGATGCCAGGGGCTCAAAGGCCAATGAC-CAGAC 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTGAGCCAGCCCAAAATGGATGAGCAGAGCCTGAGTACTTGCCGGCGGATCAGTGAGAC 1106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1167 CAGCATAGAGCCAGGGCTGGGCAAAGTCAAAGCGAGAAGCAGGTCTAACAGTGGCCTGGA 1226
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                                                                                                            747
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                                                                                               CTACATCAAAGTCACCTGGAAGAGGCTCCGCTCACATTCCAGACAGTATGTGTCCGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  315 alleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrArgArg---Gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173 GluTrpTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuLeuProValSerLeuVal
                                     748 ACCAACGGGTCCCTCCCTACCTTTTTAGAAATCAAGCTGAGGTCGGAGGATGCCAAAGAG
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                                                                                                                                                                                                       -----TrpSerLeuTrpLysArg-----
                                                                                                                                                                                                                                                                                                    868 CCTACTGGAGGTCTGGATCAGAAGTCAACATCTGAAGACCCCCAAGGTGACCTCTCCGACT
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                                                                /tissue_type="wolffian duct includes surrounding region"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="12 days embryo"
                                                                                                                                                                                                                                                                                                                 PILGWHHFTPLAPELREDKCETDFYNVTWFKIMTAIINFYLPTLLMLWFYVKIYKAVR
RHCQHRQLTNGSLPFTELEIKLRSEDBAKEGAKKFGKESPWGVOKRPSRDPTGGLDQKST
SEDFWYTSFTVFSQEGERETVTRPCFRLDVMQTQPVPEGDAKGSKANDQTLSQPKMDE
QSLGSTCRRISETSEDPGLETVRRQSFSRTTDSDTSIEPGLGKVKARSRSNSGLDYIKVTW
KRLRSHSRQYYGGLHARERKAAKQLGGIMAARILCWIPYFIPWVIAPCNSCCSEPV
HMFTIWLGYINSTLNPLIYPLCNENFKKTFKKILHIRS"
                                                                                                                                                                                                                                                                   /trānalation="MSLPNTSSASEDKMCBGNRTAMASPQLLPLVVVLSSISLVTVGL
NLLVLYAVRSERKLHTVGNLYIVSLSVADLIVGAVVMPMNILYLIMTKMSLGRPLCLF
WLSMDYVASTASIFSVFILCIDRYRSVQQPLRYLRYRTKTRASATILGAWFLSFLWVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AlavalArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAla 138
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                                                                                                                                                         'note" unnamed protein product; HISTAMINE RECEPTOR (SPTR|Q91075, evidence: FASTY, 100%ID, 100%length,
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126
80
159
118
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Mismatches:
Indels:
|mol_type="mRNA"
| errain="C57BL/GJ"
|db_xref="FaNTOM DB:6720430L06"
|db_xref="taxon:I0090"
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Matches:
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proteIn_id="BAC28011.1"
db_xref="GI:26328545"
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                                                             clone="6720430L06'
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Best Local Similarity:
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MLSMDYVASTRAIFSTRICTDRYRSVQOPLRYKTRTRASATILCAMFLSFLWVI
PILGMHFTPLAPELREDKCETDFYNVTWFKIMTAIINFYLPTLLMLMFYKIYKAVR
RHCQHRQLTNOSLPFFLEILKLRSEDAKEGAKKFGKSSPWGVQKRPSRDPTGGLDQKST
SEDPKVTSFTVFSQEGERETVTRPCFRLDVWQTQPVPBGDARGSKANDQTLSQPKMDE
GSLSTCRRISETSEDQTLVDRQFSFRTTDSDVSTEIPEGGARGSKANDQTLSQPKMDE
GRASTSTRYFSTRYFORGETTTDSDVSTEIPEGGARGSKANDGTLSQPKMDE
GRASTSTRYFSTRYFTSTRYTSDVSTEIPEGGARGSKANDGTLSQPKMDE
GRASTSTRYFYSGGGGCTRAFKKLLHTRSTRYARGKGCSEEV
HMFTIMLGYINSTLNPLIYPLCNENFKKTFKKLLHIRS"
                                                                                                                                                                                                                                                /tissue type="cerebellum"
/clone lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein id="BAC32950.1"
/db xref="GI:26338558"
/translation="MSLPNTSSASEDKMCEGNRTAMASPQLLPLVVVLSSISLVTVGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             326 GTGCGCAGTGAGCGCAAGCTACACCGTGGGCAACCTGTACATTGTCAGCCTGTCGGTA 385
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                                                                                                                                                                                                                                                                                                                   /dev_stage="10 days neonate"
173. 1639
170te="unnamed protein product; HISTAMINE RECEPTOR
(SPTR|Q91V75, evidence: FASTY, 100%ID, 100%length,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126
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Conservative:
Mismatches:
                                                                                                                                            db_xref="FANTOM_DB:B930016C09"
db_xref="taxon:10090"
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                                                                                                                                                                                                                   clone="B930016C09"
                                                                  /mol_type="mRNA"
/strain="C57BL/6J"
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/codon start=1
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                       Chordata;
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CACTTCACGCCCCTGGCCCCAGAGCTTCGGGAAGATAAGTGTGAGACAGATTTCTACAAT 730
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The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNs.

In Nature 420, 563-573 (2002)

Adachi, J., Aizawa, K., Akimura, T., Hara, A., Hashizume, W.,

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Direct Submission

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                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata: Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     URL: http://genome.gec.riken.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
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URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
                                                                                                                                                                                                                                                                                                                              cloning
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High-efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
99279253
HTC; CAP trapper.
Mus musculus (house mouse)
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RHCQHRQLTNGSLPTFLEIKLRSEDAKEGAKKPGKESPWGVQKRPSRDPTGGLDQKST
SEDPKTTSPYFSQEGRRETYTRPCFRLDVMQYDPVBEGDARGSKANDQTLSQPKNDE
QSLSTCRRISTYSEDQTLVDRQFFRTTDSDTSIEPGLGKVKARSRSNSGLDYIKYTW
KRLRSHRQYYSGLHARERKAAKQLGCIMAAFILCWIPYFIFFWVIAFCNSCCSEPV
HMFTIWLGYINSTLNPLIYPLCNBNFKKTFKKILLHIRS"
                                                                                                                                                                                                                                                                                                                                                    /translation="MGLPNTSSASEDKMCEGNRTAMASPQLLPLVVVLSSISLVTVGL
NLLVLYAVRSERKLHTVGNLYIVSLSVADLIVGAVVMPMNILYLIMTKMSLGRPLCLF
WLSMDYVASTASIFSVFILCIDRYRSVQQPLRYLRYRTKTRASATILGAWFLSFLWVI
                                                                                                                                                     /tissue type="hypothalamus"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
dev stage="adult"
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Matches:
Conservative:
Mismatches:
                                                                                    xref="FANTOM_DB:A230019E03"
xref="taxon:10090"
                                                                                                                                                                                                                                                                                                      /codon_start=1
/protein_id="BAC30013.1"
/db_xref="GI:26332591"
                                 /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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ocation/Qualifiers
                                                                                                     /db_xref="taxon:100"
/clone="A230019E03"
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QSLSTCRRISETSEDQTLVDRQSFSRTTDSDTSIEPGLGKVKARSRSNSGLDYIKVTW
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                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="adipose"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
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/db xref="FRATOM DB:B430204G09"
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/clone="B430204G09"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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Analysis of the mouse transcriptome based on functional annotation of 60,70 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3783)
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                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                  Carninci, P. and Hayashizaki, Y.
Mith-efficiency full-length cDNA cloning
Mith Enzymol. 303, 19-44 (1999)
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Mus musculus (house mouse)
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ACCESSION Mus musculus HTRIB gene, VIRTUAL TRANSCRIPT, partial sequence, ACCESSION A7415607.  VERSION A7415607.  REYNORDS SOURCE Mus musculus (house mouse) SOURCE Mus musculus (house mouse) SOURCE Mus musculus (house mouse) SOURCE Mus musculus (house mouse) SOURCE Mus musculus (house mouse) SOURCE Mus musculus (house mouse) SOURCE Mus musculus (house mouse) SOURCE Mus musculus (house mouse) SOURCE AND Mus musculus (house mouse) SOURCE AND Mus musculus (house mouse) SOURCE AND Mus musculus (house mouse) SOURCE AND Mus musculus (house mouse) SOURCE AND Mus musculus (house mouse) TITLE DIFERENCE CLark, A.G. Glanowski, S., Nielson, R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. COURNAL Solence 302 (552), 1960-1963 (2003) REFERENCE CLark, A.G. Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., TITLE DIFECT (Lark, A.G. Glanowski, S., Nielson, R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. COMMENT TITLE DIFECT SUbmission JOURNAL Submission JOURNAL Submission Location/Qualifiers  Location/Qualifiers  Location/Qualifiers  Location/Qualifiers  Location/Qualifiers  Location/Qualifiers  Mol Exper Ferancial  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene  Agene	Alignment Scores:    1.59e-27   Batches: 103   Score: 1033   Score: 104.81\$   Natches: 103   Percent Similarity: 46.81\$   Nismatches: 135   Query Match: 12.10\$   Nismatches: 159   Query Match: 19.10\$   Nismatches: 159   Query Match: 19.10\$   Nismatches: 159   Outlood: Similarity: 19.10\$   Nismatches: 159   Outlood: Similarity: 19.10\$   Nismatches: 159   Outlood: Similarity: 19.10\$   Nismatches: 159   Outlood: Similarity: 19.10\$   Nismatches: 159   Outlood: Similarity: 19.10\$   Nismatches: 159   Outlood: Outlook
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
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104 GTGATGCCCATCAGCACCATGTACACTGTCACCGGCCGCTGGACACTGGGCCAGGTGGTC
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                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/gene="HTR1B"
/locus_tag="HCM5613"
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VIRTUAL TRANSCRIPT, partial sequence,
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CTGGACTGCTTTGTGAACACCGACCACGTCCTACACGGTCTACTCCACGGTGGGCGCT 636
                                                                                                                                                                                                                                                   TICIATITACCCACCCIGCICATCATGCCCTCTATGGCCGCATCTATGGAAGCCCGC 696
                                                                                                                                                                                                                                                                                                                                                                                         225 GlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeuProGlyLeuLys 244
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                                                              147 AsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSerThrAsnThrGluGluCys 166
                                                                                                    529 TCGTTGCCACCCTTCTTC------TGCGTCAAGCCAAAGCAGAGAGAGATG 576
                                                                                                                                              GluProGlyPheValThrGluTrpTyrIleLeu-----AlaIleThrAlaPheLeuGlu 184
                                                                                                                                                                                                                            PheLeuLeuProValSerLeuValValTyrPheSerValGlnileTyrTrpSerLeuTrp 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 GluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSerLeuLeuValSer 264
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                                                                                                                                                                                                                                                                                                          LysArgGlySerLeuSerArgCysProSerHisAlaGlyPhelleAlaThrSerSerArg 224
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                868 GTCTCAGACGCCCTGCTGGAAAGAAGAACTCCATGGCCGCTAGGGAGCGCAAAGCCACC
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Science 302 (5652), 1960-1963 (2003)
14671302
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ò	224	224 ArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeuProGlyLeu 243	43
q	745		789
ò	244	244 LysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSerLeuLeuVal 263	
qq	790	790 ACGICCICGGICACTCITATIAACICGCGGGIICCCGACGIGCCCAGCGAA 84	840
È	264	SerLeuArgThrHisMetSerGlySerIleIleAlaPheLygValGlySerPheCysArg 28	283
qa	841	TATGTGAACCAAGTC 876	94
ò	284	284 SerGluserProvalLeuHisGlnArgGluHisValGluLeuLeuArgGlyArgLygLeu 303	03
qg	877	877 CGAGTCTCCGACGCCCTGCAAAAAAAAGAAACTCATGGCCGCTAGGGAGCGCAAAGCC 936	36
ò	304	laargSerLeualaValLeuLeuSerAlaPheAlaIleCysTrpAlaProTyrCysLeu 32	23
qa	937	937 ACCAAGACCTAGGGATCATTTTGGGAGCCTTTATTGTGTGTG	96
ò	324	alLeuSerThrTyrArgArgGlyGluArgProLysSerIleTrpTyrSer	343
qq	166	997 ATCTCCCTAGTGATGCCTATCTGCAAAGATGCCTGCTGGTTCCAC 1041	041
ò	344	IleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPhe 35	358
qq	1042	:::    CTAGCCATCTTTGACTTCTTCACATGGCTGGGCTATCTCAACTCCCTCATCAACCCCATA 1101	101
ò	359	JeuryrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeu 375	
qq	1102	1102 ATCTATACCATGTCCAATGAGGACTTTAAACCAGCATTCCATAAACTGATA 1152	

Search completed: August 5, 2005, 17:26:09 Job time: 3195 secs

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RYRAQHTGILKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTEECEPGFVTEWYILAIT 180
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                    version -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q91ZY3
Q865E1
HH3R_CAVPO
HH3R_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q91ZY1
Q91ZY2
Q96LD9
HH4R HUMAN
Q8WNV9
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Q8VH24
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Q22895
ACMS_HUMAN
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Maximum Match 100%
Listing first 45 summaries
                                                                                                         protein search, using sw model
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Q86GT6
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Q62M33
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Q8WXZ9
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Q6J9J4
                                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
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                       GenCore (c) 1993
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB E
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RN [1]

RC STRAIN-SPRSQUE-Dawley;

RC STRAIN-Sprsque-Dawley;

RA Liu C., Wilson S., Kuei C., Lovenberg T.W.;

Rubiu C., Wilson S., Kuei C., Lovenberg T.W.;

RL Liu C., Wilson S., Kuei C., Lovenberg T.W.;

RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

CC -!- SIMILARITY: Belongs to family 1 of G-protein (By similarity).

CC -:- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

DR GO; GO:0004081; F:receptor activity; IEA.

DR GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0001189; F:receptor activity; IEA.

DR GO; GO:0001189; F:rhodopsin-like receptor protein signalin. ..; IEA.

DR PRINTS; PR00201; GFRRHODOPSN.

DR PRINTS; PR010201; GFRRHODOPSN.

DR PRINTS; PR010201; GFRRHODOPSN.

DR PROSITE; PS50262; G-PROTEIN-RECEP FI_2; 1.

KW G-protein coupled receptor; Receptor; Transmembrane.

**ROUENCE 391 AA; 44023 MW; C707BA6E39CFED41 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DFFVGVISIPLYIPHTTENWNFGSGICMFWLITDYLLCTASVYSIVLISYDRYQSVSNAV 120
                             rattus norv
homo sapien
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                                                                                                                   gorilla gor
brachydanio
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caenorhabdi
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mus musculu
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     sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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Q81vw0 | 908483 | 908483 | 908456 | 908456 | 9094251 | 909473 | 909473 | 909473 | 909473 | 909474 | 956490 | 956490 | 956490 | 900848 | 956490 | 956490 | 956490 | 956490 | 956490 | 956490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696490 | 9696400 | 9696400 | 9696400 | 9696400 | 9696400 | 9696400 | 9696400 | 9696400 | 9696400 | 9696400 | 9696400 | 9696400 | 9696400 | 9696400 | 9696400 | 9696400 | 9696400 | 969640
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Last annotation update)
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Pred. No. 4.4e-142;
0; Mismatches 1;
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Q7T286
ACM3 MOUSE
Q6NUM3
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HH1R_HUMAN
HH1R_PONPY
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SER2 CAEEL
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  Q81VW0
ACM3_RAT
Q96RG9
Q8VH26
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Best Local Similarity 99.7
Matches 390; Conservative
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361 PLCHRRFQKAFWKILCVTKQPAPSQ-TQSVSS 391
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                                   PLCHRRPQKAFWKILCVTKQPAPSQTQSVSS 391
                                                                      361 PLCHRRFQKAFWKILCVTKQPALSQNQSVSS 391
                                                                                                                                                                                                                                                       390 AA
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MEDLINE=21106319; PubMed=11179435;
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PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01726; HISTAMINEH4R.
                                                                                                                                                                                                                                                       PRELIMINARY;
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Q96LD9;
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PGLKEPAASLHSESPRGKSSLLVSLRTHMSGSIIAFKVGSFCRSESPVLHQREHVELLRG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
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MGD; MGI:2420553; Hrh4.

MGC) GO:0005615; C:extracellular space; TAS.

MGC) GO:0005624; C:integral to plasma membrane; IC.

MGC) GO:0005624; C:immebrane fraction; IDA.

MGC) GO:00005624; P:inflammatory response; TAS.

MGC) GO:0000594; P:inflammatory response; TAS.

MGC) GO:00017 TML1;

MRINTS; PRO0127; GPCRHHOODPSN.

MRINTS; PRO0127; GPCRHHOODPSN.

MRINTS; PRO0126; HISTAMINEHAR.

MROSITE; PS502623; GPROTEIN RECEP F1 1; 1.

MG-PROLEIN COUPLED receptor; Receptor; Transmembrane.

MG-PROTEIN RECEP F1 2; 1.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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84.9%; Pred. No. 1.6e-120;
iive 17; Mismatches 42;
                                                                                                                                                                                       PLCHRRFQKAFWKILCVTKQPAPSQTQSVSS 391
                                                                                                                                                                                                                          391 AA
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Matches 332; Conservative
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01-DEC-2001 (TrEMBLrel
01-OCT-2003 (TrEMBLrel
Histamine H4 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                        Nguyen T., Shapiro D.A., George S.R., Setola V., Lee D.K., Cheng R., Rauser L., Lee S.P., Lynch K.R., Roth B.L., O'Dowd B.F.;

"Discovery of a movel member of the histamine receptor family.";

Mol. Pharmacol. 59:427-433(201).

-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

C. -1- STHILARITY: Belongs to family 1 of G-protein coupled receptors.

R. BEL, AV002280; AAL09297.1;

R. GO; GO:001681; C:integral to membrane; IEA.

GO; GO:001581; F:receptor activity; IEA.

GO; GO:0015821; F:receptor activity; IEA.

GO; GO:000188; P:redopsin-like receptor activity; IEA.

R. GO; GO:000188; P:G-protein coupled receptor protein signalin. .; IEA.

InterPro; IPR000276; GPCR Rhodpsn.

R. InterPro; IPR0002102; Histamurecept_H4.
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                                                                                                                                                      Homo sapiens (Human).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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68.7%; Score 1405.5; DB 2; Length
Best Local Similarity 69.1%; Pred. No. 1e-95;
Matches 271; Conservative 41; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00237; G PROTEIN RECEP_F1_1; 1.
PROSITE; PS0262; G PROTEIN RECEP_F1_2; 1.
G-protein coupled receptor; Receptor; Transmembrane.
SEQUENCE 390 AA: 44469 MW; CC82B5D30D216C66 CRC64;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
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'Identification of a histamine H4 receptor on human eosinophils - Role
                                                                        HH4R_HUMAN STANDARD; PRT; 390 AA.
099H3R8 / 905GOD;
16-OCT-2001 (Rel. 40, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Histamine H4 receptor (HH4R) (GPRV53) (G protein-coupled receptor 105)
(GPCR105) (SP9144) (AXOR35).
                                                                                                                                                                                                                                                                                                                       novel
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MEDLINE=21106320; PubMed=11179436;
Zhu Y., Michalovich D., Wu H.-L., Tan K.B., Dytko G.M., Mannan I.J.,
Zhu Y., Michalovich D., Wu H.-L., Li X., Herrity N.C., Vawter L.,
Sarau H.M., Ames R.S., Davenport C.M., Hieble P., Wilson S.,
Bergama D.J., Fitzgerald L.R.;
Rergama D.J., Fitzgerald L.R.;
McIoning, expression, and pharmacological characterization of a novel-
human histamine receptor.;
Mol. Pharmacol. 59:434-441(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21104636; PubMed=11181941;
Morse K.L., Behan J., Laz T.M., West R.E. Jr., Greenfeder S.A.,
Anthes J.C., Umland S., Wan Y., Hipkin R.W., Gonsiorek W., Shin N.,
Gustafson E.L., Qiao X., Wang S., Hedrick J.A., Greene J., Bayne M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning and characterization of a novel human histamine receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu C., Ma X.-J., Jiang X., Wilson S.J., Hofstra C.L., Blevitt J., Pyati J., Li X., Chai W., Carruthers N., Lovenberg T.W.; "Cloning and pharmacological characterization of a fourth histamine
                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.; "Molecular cloning and characterization of a new human histamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Leukocyte;
MEDLINE-20568725; PubMed=11118334; DOI=10.1006/bbrc.2000.4008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Jones P.G., Wu S., Betty M.;
"Cloning of a novel histamine receptor.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in eosinophil chemotaxis.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biophys. Res. Commun. 279:615-620(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   otor (H4) expressed in bone marrow.";
Pharmacol. 59:420-426(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND CHARACTERIZATION.
TISSUE=Eosinophil;
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                                                                                                                                                                                                                                          Homo sapiens (Human).
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                                                                                                                                                                                                                     Name=HRH4;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                              the
Puhl H.L. III, Ikeda S.R., Aronstam R.S.;
"cDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org)."; Submitted (JUL-2002) to the EMBL/Genbank/DDBJ databases.
-!- FUNCTION: The H4 subclass of histamine receptors could mediate thistamine signals in peripheral tissues. Displays a significant level of constitutive activity (spontaneous activity in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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PRINTS; PRO1726; HISTAMINEH4R.
PROSTIF; PS00237; G PROTEIN RECEP F1_1; 1.
PROSTIF; PS50262; G PROTEIN RECEP F1_2; 1.
G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytoplasmic (Potential).
4 (Potential).
Extracellular (Potential).
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3 (Potential).
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Cytoplasmic (Potential).
2 (Potential).
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GO; GO:0016021; C:integral to membrane; NAS.
GO; GO:0004969; F:histamine receptor activity; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR00276; GPCR Rhodpsn.
InterPro; IPR008102; Histamnrecept_H4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB044934; BAB13698.1; -. EMBL; AB045370; BAB20091.1; -. EMBL; AF307973; AAG32052.1; -.
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AAL01684.1;
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AY136745; AAN01271.1;
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PIR; JC7566; JC7566.
Genew; HGNC:17383; HRH4.
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EMBL;
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Ly C., Wilson S., Kuei C., Lovenberg T.W.;

Lu C., Wilson S., Kuei C., Lovenberg T.W.;

Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

L. SUBCELLUIAR LOCATION: Integral membrane protein (By similarity).

-!- SINGLARITY: Belongs to family 1 of G-protein coupled receptors.

RMBL; AF358858; AAK97379.1; -.

RMBL; AF358858; AAK97379.1; -.

RMBL; AF358858; AAK97379.1; -.

RMC OO; GO:0004872; F:receptor activity; IEA.

RMC OO; GO:0001584; F:rhodopsin-like receptor protein signalin. .; IEA.

RMC OO; GO:0001786; P:rhodopsin-like receptor protein signalin. .; IEA.

RMINTS; PR00237; GERRHODOPSN.

RRINTS; PR00237; GERRHODOPSN.

RRINTS; PR01726; HISTAMINEHAR.

RRINTS; PR01726; HISTAMINEHAR.

RRINTS; PR01726; GEROTEIN RECEP FI 1; 1.

RROSITE; PS50262; GEROTEIN RECEP FI 2; 1.

ROSITE; PS50262; GEROTEIN RECEP FI 2; 1.

ROSITE; PS50262; GEROTEIN RECEP FI 2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Histamine H4 receptor:
Cavia porcellus (Guinea pig).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Cavidae; Cavia.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:00016; F:G-procein coupled receptor protein signalin.
Parints; PR00237; GPCRRHODOPSN.
PRINTS; PR01726; HISTAMINEHAR.
PROSITE; PS00237; GPROTEIN RECEP F1 1; 1.
PROSITE; PS00262; GPROTEIN RECEP F1 2; 1.
G-procein coupled receptor; Receptor; Transmembrane.
SEQUENCE 390 AA; 44483 MW; BC8FD363A6F44D3F CRC64;
                                                                                                                                                             DB 2; Length 390;
                                                                                                                                                                                       96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65.0%; Score 1328.5; DB
66.9%; Pred. No. 5e-90;
iive 29; Mismatches 9
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                                                                                                                                                                                       Matches 263; Conservative
                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                179 SFLEFVIDVILVAYFNMNIYWSLWKRDHLSRCQSHPGLTAVSSNICGHSFRGRLSSRRSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RYRAQHTGILKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTEECEPGFVTEWYILAIT
                                                                                                                                                                                                                                                                                                                                                                                                         121 SYRIQHIGULKIVILMVAVWVLAFLVNGPMILUSESWKDEGS--ECEPGFFSEWYLLAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AFLEFLLPVSLVVYFSVQIYWSLWKRGSLSRCPSHAGFIATSSRGTGHSRRTGLACRTSL
                                                                                                                                                                                                                                                                         MSESNGTDVLPLTAQVPLAFLMSLLAFAITIGNAVVILAFVADRNLRHRSNYFFLNLAIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RKLARSLAVLLSAFAICWAPYCLFTIVLSTYRRGERPKSIWYSIAFWLQWFNSLINPFLY
                                                                                                                                                                                                                                                Gaps
S (Potential).

Cytoplasmic (Potential).

6 (Potential).

Extracellular (Potential).

7 (Potential).

Cytoplasmic (Potential).

By similarity.

N-linked (GlCNAC...) (Potential).

N-linked (GlCNAC...) (Potential).

N-linked (GlCNAC...) (Potential).

A -> V (in Ref. 1).

A -> V (in Ref. 1).

Q -> R (in Ref. 1).

Q -> R (in Ref. 1).

Q -> R (in Ref. 1).
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                                                                                                                                                                                                                                              ы
;
                                                                                                                                                                                                               ; Score 1403.5; DB 1; Length 390;
; Pred. No. 1.5e-95;
40; Mismatches 78; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Histanine H4 receptor.
Sus acrofa (Pig).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Bute
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLCHKRFQKAFLKIFCIKKQPLPSQHSRSVSS 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLCHRRFOKAFWKILCVTKQPAPSQ-TQSVSS 391
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                                                                                                                                                                                       44495 MW;
                                                                                                                                                                                                                  68.6%;
69.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                             Matches 271, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
  193
332
341
362
164
                                                                                                                                                                                      390 AA;
                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE PROM N.A.
 TRANSMEM
DOMAIN
TRANSMEM
                                                                                    DISULFID
CARBOHYD
CARBOHYD
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                                                                                                                                           CONFLICT
CONFLICT
CONFLICT
SEQUENCE
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                                         DOMAIN
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                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                  Local
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                                                                       DOMAIN
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                                                                                                                                                         137 VAVWILAFLVNGPMILASDSWK----NSTNTEECEPGFVTEWYILAITAFLEFLLPVSL 191
                                                                                                                                                                                                                                                                                                                                                                                                               374
                                11
                                                               96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Short; Synonyms=H3S; 180180; 18018-09J115-2; Sequence=VSP 001880; 18018-09J115-2; Sequence=VSP 001880; 18018-09J115-2; Sequence=VSP 001880; 18018-09PTICITY: Expressed in discrete neuronal populations such as brain. Highly expressed in discrete neuronal populations such as pyramidal cells in cerebral cortex or cerebellar Purkinje cells. SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
                                                 319 ------SLKRGSKPSASSASLEKRMKMVSQSFTQRPRLSRDRKVAKSLAVIVSIF
                                                                                                                                                                                                                                                                                                                                                                                                                               368 GLCWAPYTLLMIIRAAC-HGHCVPDYWYETSFWLLWANSAVNPVLYPLCHHSFRRAFTKL
                                                                                           78 F-NWNPGSGICMFWLITDYLLCTASVYSIVLISYDRYQSVSNAVRYRAQHTGILKIVAQM
                                                                                                                                                                             ----WSLWKRGSLSRCPSH
                                                                                                                                                                                                                                                     214 -VIFFNLSIYLNIQRRTRLRLDGAREAGGPEPPPEAQPSPPPPGCWGCWQKGHGEAMPLH
                                                                                                                                                                                                                                                                                  216 ------AGFIATSSRGTGHSRRTGLACRTSLPGLKEPAASLHSESPRGKSSLLV
                                                                                                                                                                                                                                                                                                                274 RYGVGEAAAGAEAGETALGGGGGGGGS----AASPTSSSG----SSSRGTERPR----
                                                                                                                                                                                                                                                                                                                                                 264 SLRTHMSGSIIAFKVGSFCRSESPVLHOR-----EHVELLRGRKLARSLAVLLSAF
                                                                                                                                                                                                                                                                                                                                                                                                             315 AICWAPYCLFTIVLSTYRRGERPKSIWYSIAFWLQWFNSLINPFLYPLCHRRFQKAFWKI
                                18 LAFLMSLLAFAITIGNAVVILAFVADRNLRHRSNYFFLNLAISDFFVGVISIPLYIPHTL
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tardivel-Lacombe J., Rouleau A., Heron A., Morisset S., Pillot C., Cochois V., Schwartz J.-C., Arrang J.-M.;
"Cloning and cerebral expression of the guinea pig histamine H3
receptor: evidence for two isoforms.";
NeuroReport 11:755-759(2000).
-!- FUNCTION: The H3 subclass of histamine receptors could mediate t.
histamine signals in CNS and peripheral nervous system. Signals through the inhibition of ademylate cyclase and displays high constitutive activity (spontaneous activity in the absence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cavia porcellus (Guinea pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.
 96;
   49; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         agonist).
SUBCELLUAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HHER CAVPO STANDARD; FRL; T.C. 195135; Q9J136; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Long; Synonyms=H3L;
IsoId=Q9JI3S-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Brain;
MEDLINE=20218440; PubMed=10757514;
                                                                                                                                                                                                                        192 WYFSVQIY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LCPOKLKIOPHSSLEO 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           375 LCVTK---QPAPSQTQ 387
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10141;
   165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=HRH3;
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   Matches
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                                                                                                                                                                                                                    AQHTGILKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTEECEPGFVTEWYILAITAFL 183
                                                                                                                                                                                                                                                                                    242
                                                                                                                                                                                                                                                                                                    241 RKETTASLGSDKSRRKSSLLFSIRAYKNSNVIASKMGFLSHSDSLALQQREHIELFRARK 300
                                                                                                                                                        VGVISIPLYIPHTLFNWNPGSGICMFWLITDYLLCTASVYSIVLISYDRYQSVSNAVRYR 123
                                                                                                                                                                          63 VGAIAIPLYIPSSLTYWTSGKQACVPWLITDYLLCTASVYNIVLISYDRYQSVSNAVWYR 122
                                                                                                                                                                                                                                                   123 AQHSGTWKIATQMVAVWIFSFMTNGPMILISDSWQNSTT--ECEPGFLKKKWYPALPTSLL 180
                                                                                                                                                                                                                                                                                                                                               LKEPAASLHSESPRGKSSLLVSLRTHMSGSIIAFKVGSFCRSESPVLHQREHVELLRGRK 302
                                                                                                                                                                                                                                                                                                                                                                                                            LARSLAVLLSAFAICWAPYCLFTIVLSTYRRGERPKSIWYSIAFWLQWFNSLINPFLYPL 362
                                                                                                                                                                                                                                                                                                                                                                                                                              63
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                                                                                                             4 SNGTDVLPLTAQVPLAFLMSLLAFAITIGNAVVILAFVADRNLRHRSNYFFLNLAISDFF
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                            .
3
                               DB 2; Length 389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 698; DB 2; Length 445;
Pred. No. 1.9e-43;
                                                            101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Receptor; Transmembrane.
SEQUENCE 445 AA; 48591 MW; E79440A4EC09CA8C CRC64;
 51AF32FD6F1C3E4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                           60.5%; Score 1237.5; DB ; 61.4%; Pred. No. 2.6e-83; ive 46; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       445 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHRRFQKAFWKILCVTKQPAPSQTQSVSS 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Macaca mulatta (Rhesus macaque).
 44511 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01471; HISTAMINEH3R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.1%;
37.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26,
                                          Local Similarity 61.4% res 239; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia, Eutheria, Prin
Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Histamine receptor H3.
 Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9544;
389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=HRH3;
                                                                                                                                                                                                                                                                                                                                                                                                                                            301
                                                                                                                                                         64
                                                                                                                                                                                                                      124
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SEQUENCE
                               Query Match
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                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F-NWNPGSGICMFWLITDYLLCTASVYSIVLISYDRYQSVSNAVRYRAQHTGILKIVAQM 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 TGRWTFGRGLCKLWLVVDYLLCTSSVFNIVLISYDRPLSVTRAVSYRAQQGDTRRAVRM 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VAVWILAFLVNGPMILASDSWK-----NSTNTEECEPGFVTEWYILAITAFLEFLLPVSL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 273 IIAPKVGSFCRSESPVLHQR------EHVELLRGRKLARSLAVLLSAFAICWAPYCL 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTIVLSTYRRGERPKSIWYSIAFWLQWFNSLINPFLYPLCHRRFQKAFWKILCVTK---Q 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VLVWVLAFLLYGPAIL---SWEYLSGGSSIPEGHCYAEFFYNWYFLITASTLEFFTPFLS 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HRYGVGEAGPGABAGEAALGGGGGAAASPTSSSGGSSSRGTERPR--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --SLKRGSKPSASSASLEKRMKMVSQSITQRFRLSRDKKVAKSLAIIVSIFGLCWAPYTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LMIIRAAC-HGHCVPDYWYETSFWLLWANSAVNPVLYPLCHYSFRRAFTKLLCPQKLKVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAFLMSLLAFAITIGNAVVILAFVADRNLRHRSNYFFLNLAISDFFVGVISIPLYLPHTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAGFIATSSRG--TGHSRRTGLACRTSLPGLKEPAASLHSESPRGKSSLLVSLRTHMSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                               PROSITE, PS0023', G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
Alternative splicing; G-protein coupled receptor; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-linked (GlcNAc. . .) (Potential)
Missing (in isoform Short).
/FTId=VSP 001880.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.1%; Score 697.5; DB 1; Length 445; 37.5%; Pred. No. 2.1e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 2.1e-43;
54; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Potential.
Extracellular (Potential).
Potential.
                                                                                                                                                                                                                                                                      Extracellular (Potential).
                                                                                                                                                                                                                                                                                                             Potential.
Extracellular (Potential).
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MW; BAE206A3887189A0 CRC64;
                                                                                                                                                                                                                                                                                                                                      Potential.
Cytoplasmic (Potential).
Potential.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytoplasmic (Potential).
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                                                                                                                              EMBL, AZ267538, AAR78950.1, -
InterPro, IPR000276, GPCR_Rhodpsn.
InterPro, IPR003980, H3_receptor.
                                                                                                                       EMBL; AF267537; AAF78947.1; -.
                                                                                                                                                                         Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01471; HISTAMINEHJR.
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Matches 159; Conservative
                                                                                                                                                                                                                                                                      445 AA;
                                                                                                                                                                                                                                                         Transmembrane
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TRANSMEM
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DOMAIN
TRANSMEM
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DOMAIN
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TRANSMEM
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CARBOHYD
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MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
MA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
A Jones M., Stavides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
A Bailey J., Barlow K.F., Bares K.N., Beard L.M., Beare D.M.,
Bailey J., Burtill W.D., Butler A.P., Carder C., Carter N.P.,
A Buck D., Burtill W.D., Butler A.P., Carder C., Carter N.P.,
Clapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
Clapman J.C., Clamp M., Clair R.E., Connor R.E., Corby N.R.,
Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
Ellington A.G., Prankland J.A., Fraser A., French L., Garner P.,
Grafham D.V., Griffiths M.N.D., Gwilliam R., Hall R.E.,
Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE_III81559; PubMed=11284713; DOI=10.1042/0264-6021:3550279; Coge F., Guenin S.-P., Audinot V., Renouard-Try A., Beauverger P., Macia C., Ouvry C., Nagel N., Rique H., Boutin J.A., Galizzi J.-P.; "Genomic organization and characterization of splice variants of the human histamine H3 receptor.";
                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION.
MEDLINE=20568725; PubMed=11118334; DOI=10.1006/bbrc.2000.4008;
Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.;
"Molecular cloning and characterization of a new human histamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT SHY-DRAGER SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-21953383; PubMed=11956964; DOI=10.1007/s007020200036; Wiedemann P., Boenisch H., Oerters F., Bruess M.; "Structure of the human histamine H3 receptor gene (HRH3) and identification of naturally occurring variations."; J. Neural Transm. 109:443-453(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 3).
Ullmer C., Zirwes E., Lubbert H.;
"Cloning and functional expression of the human histamine H3S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIINE=99278519; PubMed=10347254; Lovenberg T.W., Roland B.L., Wilson S.J., Jiang X., Pyati J., Huvar A., Jackson M.R., Erlander M.G.; "Cloning and functional expression of the human histamine H3
                                                                                                                                                     HH3R HUMAN STANDARD, PRT; 445 AA.
Q9YSZI; OGGZZ2; Q9H4K8;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Histeranine H3 receptor (HH3R) (G protein-coupled receptor 97)
Hommon Sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor, HH4R.";
Biochem. Biophys. Res. Commun. 279:615-620(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mol. Pharmacol. 55:1101-1107(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1).
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PAPS 384
                                          436 PHSS 439
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381
                                                                                                                                       HUMAN
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-1- TISSUE SPECIFICITY: Expressed predominantly in the CNS, with the greatest expression in the thalamus and caudate nucleus. The various isoforms are mainly coexpressed in brain, but their relative expression level varies in a region-specific manner. Isoforms 3 and 7 are highly expressed in the thalamus, caudate nucleus and cerebellum while isoforms 5 and 6 show a poor expression. Isoforms 5 and 6 show a high expression in the amygdala, substantia nigra. Greek and special cortex and hypothalamus. Isoform 7 is not found in hypothalamus or substantia nigra.
-!- DISEASE: Defects in HRH3 are a cause of SNy-Drager syndrome (MIM:146500). This syndrome is characterized by orthostatic hypothension, bladder and bowel incontinence, anhidrosis, iris atrophy, amystrophy, ataxia, rigidity and tremor.
-!- MISCELLANEOUS: Does not bind to cimetidine and tripolidine. Shows modest affinity for thioperamide, imetit, N-alpha-methylhistamine and R(-)-alpha-methylhistamine isoform 4 is unable to bind to idodoproxyfan while isoforms 1 and 3 bind it with high affinity.
-!- SIMILANITY: Belongs to the G-protein coupled receptor 1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The DNA sequence and comparative analysis of human chromosome 20.", Nature 414:865-871(2001).
-!- FUNCTION: The H3 subclass of histamine receptors could mediate the histamine signals in CNS and peripheral nervous system. Signals through the inhibition of adenylate cyclass and displays high constitutive activity (spontaneous activity in the absence of agonist). Agonist stimulation of isofoxm 3 niether modified
Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., Lehvaeslaino M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A., Mistry D., Moromachie L.J., McJacy K., McMurray A.A., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Phillimore B.J.C.T., Prathalingan S.R., Plumb R.W., Ramsay H., Rice C.M., Ross M.T., Socht C.E., Sehra H.K., Shownkeen R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E., Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Whittaker P., Williams L., Williams S.A., Wilmig L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                agonist). Agonist stimulation of isoform 3 niether modified adenylate cyclase activity nor induced intracellular calcium mobilization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLUTAR LOCATION: Integral membrane protein. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=7;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q9Y5N1-2; Sequence=VSP_001886;
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AJ296652; CAC51025.1; AJ278250; CAC39434.1; AL078633; CAC04014.1;

EMBL; EMBL; EMBL; EMBL;

AB045369; AB019000;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 VAVWILAFLVNGPMILASDSWK----NSTNTEECEPGFVTEWYILAITAFLEFLLPVSL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0001887; P:histamine receptor activity; TAS.
GO; GO:0001187; P:G-protein signaling, coupled to cyclic nucl. ..; TAS.
GO; GO:0007269; P:neurotransmitter secretion; TAS.
InterPro; IPR00276; GPCR_Rhodpsn.
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                                                                                                                                                                        PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
Alternative splicing; Disease mutation; G-protein coupled receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K -> KKONKKKCL (in isoform 2).
/FIId=vSP 001886.
A -> V (in Shy-Drager syndrome).
/FIId=vAR 012235.
E -> D (in Ref. 1 and 5).
W; ZACF7440FBE95B6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.9%; Score 693; DB 1; Length 445; 37.6%; Pred. No. 4.5e-43;
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                                                                                                                                                                                                                                                                         Potential.
Extracellular (Potential)
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Cytoplasmic (Potential).
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(in isoform 6).
SP 001883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (In isoform 7).
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Missing (in isoform 3).
/PTId=VSP 001885.
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EMBL; AF363791; AAK50040.1; -.
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PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01471; HISTAMINEH3R.
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445 AA;
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Best Local Similarity
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                       MIM; 604525; -.
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97 TGRWTFGRGLCKLWLVVDYLLCASSVFNIVLISYDRFLSVTRAVSYRAQQGDTRRAVRKM 156
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                                                                                                                                                                                                              37 LAALMALLIVATVIGNALVMLAFVADSSLRTQNNFFLLNLAISDFLVGAFCIPLYVPYVL 96
                                                                                                                                                                                                                                                                                                                                             157 ALVWVLAFLLYGPAIL---SWEYLSGGSSIPBGHCYABFFYNWYFLITASTLEFFTPFLS
                                                                                                                                                                                                                                                                                                                                                                                              334 EKRMKMVSQSI-----TQRFRLSRDKKVAKSLAIIVSIFGLCWAPYT
                                                                                                                                                                                                                                                                                                                 137 VAVWILAFLVNGPMILASDSWK-----NSTNTEECEPGFVTEWYILAITAFLEFLLPVSL
                                                                                                                                                                                                                                                                                                                                                                           192 VVYFSVQIY-----WSLWKRGSLSRCPSH
                                                                                                                                                                                                                                                                                                                                                                                                                                      216 -----AG-FIATSSRGTGHSRRTGLACR-----TSLPGLKEPAASLHSESPRGKSSLL
                                                                                                                                                                                              18 LAFLMSLLAFAITIGNAVVILAFVADRNLRHRSNYFFLNLAISDFFVGVISIPLYIPHTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Morisset S., Rouleau A., Ligneau X., Gbahou F., Tardivel-Lacombe J., Stark H., Schunack W., Ganellin C.R., Schwartz J.-C., Arrang J.-M.;
                                                                                        (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lovenberg T.W., Pyati J., Chang H., Wilson S.J., Erlander M.G. "Cloning of rat histamine H3 receptor reveals distinct species
                                                                                                                                 33.5%; Score 686; DB 1; Length 445; 37.1%; Pred. No. 1.5e-42; tive 49; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Striatum;
MEDLINE=21016732; PubMed=11130725; DOI=10.1038/35048583;
                            Extracellular (Potential)
                                                                      Poly-Ala.
N-linked (GlCNAc. ..) (Poly-BBD406E29E1F3C5F CRC64;
                                                           Cytoplasmic (Potential).
Cytoplasmic (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HH3R RAT STANDARD; PRT; 445 AA. Q9QYNS; Q9QYNS; Q9QYNS; Q9QYNS; Q8-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) Histamine H3 receptor (HH3R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pharmacological profiles.";
J. Pharmacol. Exp. Ther. 293:771-778(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                             Potential
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MEDLINE=20330707; PubMed=10869375;
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445 AA;
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159; Conserv
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                             318
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                                                                                                                                      :||||| |::| | ::|| |: 368 GLCWAPYTLLMIRAAC-HGHCVPDYWYETSFWLLWANSAVNPVLYPLCHHSFRRAFTKL 426
------AGFIATSSRGTGHSRRTGLACRTSLPGLKEPAASLHSESPRGKSSLLV 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning of mouse histamine H3 receptor.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: The H3 subclass of histamine receptors could mediate the histamine signals in CNS and peripheral nervous system. Signals through the inhibition of adenylate cyclase and displays high constitutive activity (spontaneous activity in the absence of agonist) (By similarity).
-!- SUBCELULIAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
                  274 RYGVGEAAVGAEAGEATLGGGGGGS----VASPTSSSG----SSSRGTERPR-----
                                                                         315 AICWAPYCLFTIVLSTYRRGERPKSIWYSIAFWLQWFNSLINPFLYPLCHRRFQKAFWKI
                                                         264 SLRTHMSGSIIAFKVGSFCRSESPVLHQR-----EHVELLRGRKLARSLAVLLSAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAN=CD-1,
Coge F., Rique H., Levacher B., Leopold O., Guenin S.-P., Boutin J.A.
Galizzi J.-P.;
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01471; HISTAMINEH3R.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; GPROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Glycoprotein; Transmembrane.
DOMAIN
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Cytoplasmic (Potential).
Potential.
Extracellular (Potential).
Potential.
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Last annotation update)
                                                                                                                                                                                                                                                                                     445 AA
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InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR003980; H3_receptor.
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                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last seq
                                                                                                                                                                                                                                                                                                                                             25-OCT-2004 (Rel. 45, Last and Histamine H3 receptor (HH3R).
                                                                                                                                                                              375 LCVTK---QPAPS 384
                                                                                                                                                                                                          427 LCPQKLKIQPHSS 439
                                                                                                                                                                                                                                                                                     STANDARD;
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25-OCT-2004
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                                                                                                                                                                                                      FUNCTION: The H3 subclass of histamine receptors could mediate the histamine signals in CNS and peripheral nervous system. Signals through the inhibition of adenylate cyclase and displays high constitutive activity (spontaneous activity in the absence of
constitutive activity of native H3 receptors regulates histamine
                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q9QYN8-4; Sequence=VSP_001888, VSP_001889;
TISSUE SPECIFICTTY: Expressed abundantly in brain, most notably throughout the thalamus, the ventromedial hypothalamus and the caudate nucleus. Isoform i is largely predominant in all tissues. MISCELLANEOUS: Proxyfan acts as a potent neutral antagonist while thioperamide, ciproxifan and FUB465 act as potent inverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
Alternative splicing; G-protein coupled receptor; Glycoprotein;
                                                                                                  [4]
TISSUE SPECIFICITY.
MEDLINE=99278519; PubWed=10347254;
Lovenberg T.W., Roland B.L., Wilson S.J., Jiang X., Pyati J.,
Huvar A., Jackson M.R., Erlander M.G.;
"Cloning and functional expression of the human histamine H3
                                                SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4). Itadami H., Takkimura T., Nakamura T., Ohta M.; "Cloning of a novel g protein-coupled receptor."; submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
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Cytoplasmic (Potential)
Potential.
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Cytoplasmic (Potential).
Potential.
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                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=4; Comment=Additional isoforms seem to exist;
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                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q9QYN8-3; Sequence=VSP_001888;
                                                                                                                                                                                                                                                                                                                        Name=1; Synonyms=H3L;
IsoId=Q9QYN8-1; Sequence=Displayed;
Name=2; Synonyms=H3S;
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InterPro; IPR00276; GPCR_Rhodpsn.
InterPro; IPR003980; H3_receptor.
Pfam, PF00001; 7tm l1. Treceptor.
PRINTS; PR00237; GPCRHODOPSN.
PRINTS; PR01471; HISTAMINEH3R.
                                                                                                                                                                               receptor.";
Mol. Pharmacol. 55:1101-1107(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AF237919, AAF82086.1, -.
EMBL, AY009370, AAK02069.1, -.
EMBL, AB015646, BAA88765.1, -.
EMBL, AB015646, BAA8876.1, -.
EMBL, AB015646, BAA88767.1, -.
EMBL, AB015646, BAA88767.1, -.
                         Nature 408:860-864(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 AGFIATSSRGT-----GHSRRTGLACRTSLPGLKEPAASLHSESPRGKSSLLVSLRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268 HMSGSIIAFKVGSFCRSESPVLHQR-----EHVELLRGRKLARSLAVLLSAFAICW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | | | : | | : | | : | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gape
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Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPAEPRQLLLPAPPPGLGRWPCPACPVCTIRIWGWVVMG
                                                                                                                                                                                                                                                                      (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88;
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
SI:bZ34G2.4 (Novel protein similar to human histamine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.3%; Score 682; DB 1; Length 44 37.0%; Pred. No. 2.9e-42; Live 51; Mismatches 133; Indels
   Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FTId=VSP_001889.
63DFEFC21758FE5B_CRC64;
                                                                                                                                   Extracellular (Potential)
                                                                 Cytoplasmic (Potential).
                                                                                                                                                                                                                                                               N-linked (GlcNAc. .)
Missing (in isoform 2).
/FIId=VSP_001887.
                                                                                                                                                                                                    Cytoplasmic (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                473 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      445 AA; 48588 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             379 K---QPAPSQTQ 387
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   DOMAIN
TRANSMEM
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TRANSMEM
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246 -PAASLHSESPRGKSSLLVSLRTHMSGSIIAFKVGSPC-----RSESPVLHQREHVEL 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. Subcellular Locations of the number of the subceptor. Fig. 1. Neuropharmacology 0:0-0(2002).

1. Subcellular Locations integral membrane protein (By similarity).

2. -1-Subcellular Locations to family 1 of G-protein coupled receptors. Rembi, AF21911; AAL71912.1; -1-Subcellular Locations in Embi, AF21911; AAL71912.1; -1-Subcellular Locations in Embi, AF21911; AAL71912.1; -1-Subcellular Locations in Embi, AF21911; AAL71912.1; -1-Subcellular Coupled receptor activity; IEA.

GO; GO:0004869; F:histamine receptor activity; IEA.

GO; GO:000186; P:G-protein coupled receptor protein signalin. .; IEB.

RO; GO:0001158; P:nhodopain-like receptor protein signalin. .; IEB.

RO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEB.

RR PROSITE; PRO0237; GPROTEIN RECEP F1.1; 1.

R PROSITE; PRO0237; GPROTEIN RECEP F1.2; 1.

G-protein coupled receptor; Receptor; Transmembrane.

G-protein coupled receptor; Receptor; Transmembrane.

G-protein Signal May, D78832042464CB35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 VAVWILAFLVNGPMILASDSWK----NSTNTEECEPGFVTEWYILAITAFLEFLLPVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 P-NWNPGSGICMFWLITDYLLCTASVYSIVLISYDRYQSVSNAVRYRAQHTGILKIVAQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 LLVWVLAFLLYGPAIL---SWEYLSGGSSIPEGHCYAEFFYNWYFLITASTLEFFTPFLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192 VVYFSVQIYWSLWKRGSLSRCPSHAGFIATSSRGTGHSRRTGLACRTSLPGLKE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214 VIFFNLSIYLNI---------QRRT----RLRLDGAREAAGPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 LAFLMSLLAFAITIGNAVVILAFVADRNLRHRSNYFFLNLAISDFFVGVISIPLYIPHTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90; Gaps
                                                                                                              Brann M.R.,
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                               "Molecular Cloning and Characterization of Functionally Distinct Isoforms of the Human Histamine H3 Receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            y Match 32.2%; Score 658; DB 2; Length 36: Local Similarity 39.0%; Pred. No. 1.4e-40; nes 152; Conservative 44; Mismatches 104; Indels
                                                                                                       Wellendorph P., Goodman M.W., Burstein E.S., Nash N.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             373 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Histamine H3 receptor isoform 4.
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                                                                            TISSUE=Hippocampus;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271 LRSFKMKPLGAGDVQRVFFV----RPVBESRVADLASRSRCCRLASTAKVSAAEFGNGRQ 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254 SPRGKSSLLVSLRTHMSGSIIAFKVGSF---CRSESPVLHQREHV-----ELLRGRKL 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRHRSNYFFLNLAISDFFVGVISIPLYIPHTLF-NWNPGSGICMFWLITDYLLCTASVYS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 LRTQGNFFFLNLAIADFLVGGFCIPVYIPYVLTGEWRLGRGLCKLWLVVDYMLCTASVFN 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 IVLISYDRYQSVSNAVRYRAQHTGILK-IVAQMVAVWILAFLVNGPMILASDSWKNSTNT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207 -GSLSRCPSHAG-----FIATSSRGTGHSRRTGLACRISLPGL----KEPAASLHS--E 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    327 SKRRDSTLADLPPLQVEERILAASEAQFHYVDHSAGPHRHRPDMVASLANRFRLSRDKKV 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304 ARSLAVLLSAFAICWAPYCLFTIVLSTYRRGERPKSIWYSIAFWLQWFNSLINPFLYPLC 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94
                                                                                                                                                                                                                                                                                                                                                                                                                                                    .; IEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 E-----ECEPGFVTEWYILAITAPLEFLLPVSLVVYPSVQIYWSLWKR------
                                                                                               Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
--- SUBCELLULAR LOCATION: Integral membrane protein (By similarity)
--- SUBILARITY: Belongs to family 1 of G-protein coupled receptors.
EMBL, AL928906; CAR49238.1; --
ZFIN; ZDB-GRNE-040724-204; sl:rp71-34g2.4.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:000184; F:rhodopsin-like receptor activity; IEA.
GO; GO:000186; B:G-protein coupled receptor protein signalin. .;
InterPro; IPR00360276; GPCR_Rhodosn.
InterPro; IPR00360276; GPCR_Rhodosn.
InterPro; IPR00360376; GPCR_Rhodosn.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.8%; Score 671; DB 2; Length 473; 38.1%; Pred. No. 2e-41; tive 60; Mismatches 143; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam, PP00001, 7tm 1, 1.

PRINTS; PR00237, GPCRRHODOPSN.

PRINTS; PR01471; HISTAMINBHSN.

PROSITE, PS00267, G_PROTEIN_RECEP_F1_1, 1.

PROSITE, PS00262, G_PROTEIN_RECEP_F1_2, 1.

G-protein coupled receptor; Receptor; Transmembrane.

SEQUENCE 473 AA; 53506 MW; 032FC7C27DBC6E57 CRC64;
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1-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Histamine H3 receptor isoform 2
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|HSSFKRAFSKLLC-----PSKTK 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 38.1
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                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 VAVWILAFLVNGPMILASDSWK----NSTNTEECEPGFVTEWYILAITAFLEFLLPVSL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLVWVLAFLLYGPAIL---SWEYLSGGSSIPEGHCYAEFFYNWYFLITASTLEFFTPFLS 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246 -PAASLHSESPRGKSSLLVSLRTHMSGSIIAPKVGSFC-----RSESPVLHQREHVEL 297
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Wellendorph P., Goodman M.W., Burstein E.S., Nash N.R., Brann M.R., Weiner D.M., "Molecular Cloning and Characterization of Functionally Distinct Isoforms of the Human Histamine H3 Receptor.";
                                                             Neuropharmacology 0:0-0 (2002).

--- SUBCELLULAR LOCATION: Integral membrane protein (By similarity)
--- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

SMELLARITY: Belongs to family 1 of G-protein coupled receptors.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0004969; F:histamine receptor activity; IEA.

GO; GO:0004969; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001864; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001865; F:rhodopsin-like receptor activity; IEA.

Frank, PRO001; †m. 1; 1.

PRINTS; PR00237; GFCRRHODPSN.
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Ban troglodytes (Chimpanzee).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                                                                                                                                                                                                                 32.2%; Score 658; DB 2; Length 373; llarity 39.0%; Pred. No. 1.4e-40; Conservative 44; Mismatches 104; Indels
                                                                                                                                                                                                                                                                             PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Receptor; Transmembrane.
SEQUENCE 373 AA; 41570 MW; PAE9DPC5C3AP4DE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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Genome Res. 14:845-851(2004)
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060305
AC 0603045;
DT 05-JUL-;
DT 05-JUL-;
DE Histamin
OC Eukaryol
OC Eukaryol
OC Rammalia
OC NOBL Tain
RN (1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                269 MSGSIIAFKVGSFCRSESPVLHQREHVELLRGRKLARSLAVLLSAFAICWAPYCLFTIVL 328
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EMBL; AY561469; AAT45507.1; -.
GO; GO:0016021; C:integral to membrane; IBA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IBA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin.
InterPro; IPR00276; GPCR_Rhodpsn.
InterPro; IPR008102; Histamnrecept_H4.
Pfam; PF00001; 7tm 1; 1.
Pfam; PF00001; All 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 SFYSSATGPKSVWYRIAFWLOWFNSFVNPLLYPLCHKRFOKAFLKIFCIKKOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47; Indels
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19824 MW; E5961FDAC315182F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
28.2%; Score 577; DB 2;
Best Local Similarity 64.7%; Pred. No. 6.3e-35;
Matches 112; Conservative 14; Mismatches 47;
                                                                                                                                                                                                                                                                                             PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1
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175 1
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